

125082

From: Hamud, Fozia  
Sent: Tuesday, December 27, 2005 12:34 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 10/691,923

Hello,  
Kindly search SEQ ID NO:34 of 10/691,923 against commercial and interference data bases. Thank you.

FOZIA HAMUD  
PATENT EXAMINER  
ART UNIT 1647  
ROOM:REM 4D64  
MAIL BOX: REM 4C70

URFF

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA#: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 29, 2005, 13:46:42 ; Search time 227 Seconds

Title: US-10-691-923-34  
 Perfect score: 955  
 Sequence: 1 MGIVPTSKPTTIGKCHIGR.....LKVADGNLSLRSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing First 45 summaries

Database : UniProt 05.80;\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	99.0	200	1 IL29_HUMAN	Q8iu54 homo sapien
2	667	69.9	200	1 IL28B_HUMAN	Q8iz19 homo sapien
3	653	68.4	200	1 IL28A_HUMAN	Q8iz20 homo sapien
4	477	49.9	193	2 Q4VK74_MOUSE	Q4vk74 mus musculus
5	463	48.5	193	2 Q4VK73_MOUSE	Q4vk73 mus musculus
6	458	48.0	193	1 IL28_MOUSE	Q8cjkg6 mus musculus
7	97.5	10.2	692	1 PPK_ACIBA	Q9x4m8 acinetobact
8	89.5	9.4	914	2 Q4ZV84_PSEUDOMONAS	"IL-28B, IL-29 and their class II cytokine receptor IL-28R."
9	89	9.3	296	2 Q8G5G0_BIFIDOBACTERIUM	Q8g5g0 bifidobacterium
10	89	9.3	458	2 Q8DJL0_SYNEL	Q8dj10 synechococcus
11	88.5	9.3	313	2 Q75BW8_ASHGGO	Q75bw8 asbya gooss
12	87.5	9.2	953	2 Q6FCX8_ACIDABACTER	Q6fcx8 acinetobact
13	87	9.1	479	2 Q7OZJB_GIALIA	Q7qzj8 giardia lam
14	86.5	9.1	967	2 Q5b9M4_EMENI	Q5b9m4 aspergillus
15	86	9.0	333	2 Q5D4G6_BOVINUS	Q5bd6 bos taurus
16	86	9.0	528	2 Q4KB02_PSEIFIS	Q4kb02 pseudomonas
17	86	9.0	567	2 Q5BA80_ACIDABACTER	Q5ba80 acinetobact
18	85.5	9.0	574	2 Q52GV5_MAGGR	Q52gv5 magnaporthe
19	85.5	9.0	2173	2 Q4Q895_LEIMA	Q4q895 leishmania
20	85	8.9	673	2 Q57PJS_SALCHIA	Q57pj5 salmonella
21	85	8.9	975	2 Q4O6E0_LEIMA	Q4q6e0 leishmania
22	84.5	8.8	371	2 Q6SP70_ARABIDOPSIS	Q6sp70 arabidopsis
23	84.5	8.8	455	2 Q9SG79_ARAFERIA	Q9sg79 araferia
24	84.5	8.8	881	2 Q6OAC8_METACA	Q6oac8 metacaspase
25	84.5	8.8	918	2 Q884J3_PSEUDOMONAS	Q884j3 pseudomonas
26	84.5	8.8	1122	2 QBJAV1_9RETROVIRUS	Qbjav1 9retrovirus
27	84.5	8.8	1799	1 DOCK8_HUMAN	Q5jk8 human
28	84.5	8.8	2032	2 Q5JPJI_HUMAN	Q5jpj1 human
29	84	8.8	204	2 Q8BN24_PSEUDOMONAS	Q8bn24 pseudomonas
30	84	8.8	663	2 Q9NV65_HUMAN	Q9nv65 human
31	84	8.8	1379	2 Q7QEKS_ANOGA	Q7qeks anopheles g

RESULT 1					
IL29_HUMAN STANDARD ; PRT ; 200 AA.					
ID	IL29_HUMAN				
AC	Q8IU54;				
DT	01-FEB-2005	(Rel. 46, Created)			
DT	01-FEB-2005	(Rel. 46, Last sequence update)			
DT	13-SEP-2005	(Rel. 48, Last annotation update)			
DE	Interleukin 29 precursor (IL-29) (Interferon lambda-1)	(IFN-lambda-1)			
DE	(Cytokine Zcyt021).				
DN	Name=IL29, Synonyms=IFNL1, ZCYT021;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.				
OC					
OX	NCBI_TaxID=9606;				
RN					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	PubMed=12469119; DOI=10.1038/nature0873;				
RA	Sheppard P., Kindvogel W., Xu W., Henderson K., Schlutsmeyer S., Whitmore T.E., Kuesterer R., Garrigue U., Birks C., Roraback J., Cooper E., Taitt D., Shin J., Presnell S., Fox B., Haldeman B., McKnight G., Clegg C., Foster D., Klucher K.M.; "IL-28, IL-29 and their class II cytokine receptor IL-28R."; Nat. Immunol. 4:63-68 (2003).				
RN					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	DOI=10.1038/nature0873;				
RA	Kotanko S.V., Gallagher G., Baurin A., Lewis-Antes A., Shen M., Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.; "IFN-lambda mediates antiviral protection through a distinct class II cytokine receptor complex"; Nat. Immunol. 4:69-77 (2003).				
RN					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	MEDLINE=2238857; PubMed=1247793; DOI=10.1073/pnas.242603899;				
RA	Klauser R.D., Collins P.S., Wagner L., Schuler G.D., Schuler G.D., Aebischer P.D., Buetow K.H., Sherman C.M., Derge J.G., Hopkins R.F., Zeeberg B.R., Bhat N.K., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.B., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulhall S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Liu X., Gibbs R.A.,				

FAHEY J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., Schnierch A., Schein J.E., Jones S.J.M., Marrs M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Cytokine with immunomodulatory activity. May play a role in antiviral immunity. Up-regulates MHC class I antigen expression. Ligand for the heterodimeric class II cytokine receptor composed of IL10RB and IL28RA. The ligand/receptor complex seems to signal through the Jak-STAT pathway.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- INDUCTION: By viral infections or double stranded RNA.

CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.

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CC -!- EMBL; AY129150; ANR28265.1; - mRNA.

CC -!- DR EMBL; AY134372; ANR88125.1; - mRNA.

CC -!- DR EMBL; AY1336716; AAR24511.1; - mRNA.

CC -!- DR EMBL; BC074985; AAT74985.1; - mRNA.

CC -!- DR Ensembl; ENSG00000182393; Homo sapiens.

CC -!- DR HGNC; HNCI:183163; IL29.

CC -!- DR MIM; 607403; .

CC -!- DR SIGNAL; 1 19

CC -!- FT CHAIN 20 200

CC -!- FT CARBOHYD 65 65

CC -!- SQ SEQUENCE 200 AA; 21898 MW; D4333B9462DCB4A1 CRC64;

CC -!- Query Match Score 94%; Pred. No. 2.4e-78; Length 200; Best Local Similarity 99.4%; Mismatches 0; Indels 0; Gaps 0; Matches 180; Conservative 0;

Qy 2 GPVPTSKPRTTGKGCHIGRKFLSLSPOELASPKARDALLESLKLKNWCSSPVFPGNMDL 61

Db 20 GPVPTSKPRTTGKGCHIGRKFLSLSPOELASPKARDALLESLKLKNWCSSPVFPGNMDL 79

Qy 62 RLLQYRERPVALAEALALTIVKLEAAAGPALEVDQPHTLHILSQACIOQPTAG 121.

Db 80 RLLQYRERPVALAEALALTIVKLEAAAGPALEVDQPHTLHILSQACIOQPTAG 139

Qy 122 PPRPGRPLHHMLQBAPIKESAGLEASAGLEAVSVTENPLRLKVDAGNLSLRSTHPS 181

Db 140 PRPRGRLHHMLQBAPIKESAGLEASAGLEAVSVTENPLRLKVDAGNLSLRSTHPS 199

Qy 182 T 182

Db 200 T 200

Qy RESULT 2

IL28B HUMAN

ID TI28B\_HUMAN STANDARD PRT; 200 AA.

AC Q8I2I9; Q6VN55; Q724J3; Q8IWL6;

DT 01-FEB-2005 (Rel. 46, Created)

DT 13-SEP-2005 (Rel. 48, Last sequence update)

DE Interleukin 28B Precursor (IL-28B) (Interferon lambda-3)

DE (IFN-lambda-3) (Interferon lambda-4) (Cytokine ZC1022).

DE Name=IL28B; Synonym=IFNL3, IFNL4, IL28B, CYTO22;

OS Homo sapiens (Human).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Qy Query Match Score 66.5%; DB 1; Length 200; Best Local Similarity 76.6%; Pred. No. 6.3e-53; Matches 134; Conservative 11; Mismatches 25; Indels 5; Gaps 2;

Qy 2 GPVPTSKPRTTGKGCHIGRKFLSLSPOELASPKARDALLESLKLKNWCSSPVFPGN 58

Db 24 GAVPVARLGALPDARGCHIAQPKFLSPOELASPKARDALLESLKLKNWCSSPVFPGN 83

Qy 59 WDLRQLQVRPVVALAEALALTIVKLEAAAGPALEVDQPHTLHILSQACIOQ 116

Db 84 WDLRQLQVRPVVALAEALALTIVKLEATDPLGDVLDQPLHTLHILSQACIOQ 143

Db	144	QPTAGPRTRGRLUHHLRQLQEAPRKESSEVTFNLFRLTRDNCVASGDL	198	Query Match Score 68.4%; Best Local Similarity 74.9%; Pred. No. 1.2e-51; Matches 131; Conservative 13; Mismatches 26; Indels 5; Gaps 2;
<b>RESULT 3</b>				
IL28A HUMAN	STANDARD;	PRT;	200 AA.	Qy 2 GPVPTSK--PPTGKGCHIGRFKLSPOELASFKKDALARLQKNSCSPVFPGSN 58
ID Q6VNS55; Q8IWL7;				Db 24 GAVPVARLHGALPDARGHIAQFKSLSPQELQAFKRDALBESLUDCRCSRLFPP 83
AC 08IZJ0; 06VNS55; Q8IWL7;				Qy 59 WDLRQLQYERPEVLAELBLTLKVLFAAA-GPALEDPVLDQPLHTLHHIISQLQACQP 116
DT 01-FEB-2005 (Rel. 46, Last sequence update)				Db 84 WDLRQLQYERPEVLAELBLTLKVLQATADTDPLVLDQPLHTLHHIISQLQACQP 143
DT 13-SEP-2005 (Rel. 48, Last sequence update)				Qy 117 QPTAGPRPRGRLLHHTLHLRQLQPKESAGCLEASFTNLFRLLTDLKVKVADGN 171
DE Interleukin 28A Precursor (IL28A) (Interferon lambda-2) (IFN-lambda-2)				Db 144 QPTAGPRPRGRLLHHTLHLRQLQPKESAGCLEASFTNLFRLLTDLKVKVADGN 198
DN (Cytokine ZCYT020)				
GN Name=IL28A; Synonyms=IFNL2, ZCYT020;				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.				RESULT 4
RX PubMed=12469119; DOI=10.1038/nature073;				Q4VK74_MOUSE
RA Sheppard P., Kindvogel W., Xu W., Henderson K., Schlutzmeyer S.,				ID Q4VK74_MOUSE PRELIMINARY;
RA Whitmore T.E., Kuestner R., Barrigues U., Birris C., Rottback J.,				AC Q4VK74;
RA Ostrander C., Dong D., Shin J., Presenelli S., Fox B., Haldeman B.,				DT 13-SEP-2005 (TREMBLrel. 31, Created)
RA Cooper E., Taft D., Gilbert T., Grant F.J., Tackett M., Krivan W.,				DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
RA McKnight G., Clegg C., Foster D., Klucher K.M.; Nat. Immunol. 4:63-68(2003).				DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
RA "IL-28, IL-29 and their class II cytokine receptor IL-28R.";				DE Interferon-lambda2.
RA Nucleotide Sequence of 5'-200, Function, Subcellular Location, and				GN Name=ifnl2;
RP INDUCTION.				OS Mus musculus (Mouse).
RX PubMed=12483210; DOI=10.1038/nature075;				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA Korenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,				OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;
RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.,				OC Muridae; Murine; Mus;
RT "IFN-lambdas mediate antiviral protection through a distinct class II				OX NCBI_TaxID=10090;
CC cytokine receptor complex.";				RN [1]
RL Nat. Immunol. 4:69-77(2003).				RP NUCLEOTIDE SEQUENCE.
RN				RC STRAIN=129/Sv;
RP NUCLEOTIDE SEQUENCE OF 4-200.				RX PubMed=15948336; DOI=10.1099/vir.0.80904-0;
RA Li M., He S., RT "Construction of mammalian cell expression vector of human interleukin				RA Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.;
RT (IL)-28A, IL-28B and IL-29 gene from activated peripheral blood				RT Murine interferon lambdas (type III interferons) exhibit potent
RT mononuclear cell and analysis of its sequence.";				RT antiviral activity in vivo in a poxvirus infection model.";
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.				RL J. Gen. Virol. 86:1589-1596 (2005).
CC - FUNCTION: Cytokine with immunomodulatory activity. May play a role				DR AY86695; AAX58714-1; MW: 21713 MW;
CC in antiviral immunity. Up-regulates MHC class I antigen				SQ SEQUENCE 193 AA; CRC64;
CC expression. Ligand for the heterodimeric class II cytokine				Query Match Score 49.8%; Best Local Similarity 60.0%; Pred. No. 1.7e-35;
CC receptor composed of IL10RB and IL28RA. The ligand/receptor				Matches 102; Conservative 18; Mismatches 48; Indels 2; Gaps 2;
CC complex seems to signal through the Jak-STAT pathway.				Qy 3 PVP-TSKPTTGKGCHIGRFKLSPOELASFKKDALARLQKNSCSPVFGNWL 61
CC - SUBCELLULAR LOCATION: Secreted.				Db 21 PVPATRLPVEAKDCHIAQFKSLSPQELQAFKKAQDIAEKLLEDMRCSSHLSRAWDL 80
CC -- INDUCTION: By viral infections or double stranded RNA.				Qy 62 RLLQYERPEVLAELBLTLKVLFAAAQSKETPQPLHTLHHIISQLQACIQPQPTAG 121
CC -- SIMILARITY: It belongs to the IL-28/IL-29 family.				Db 81 KQLQYQBRPKLQAEVALTKWBNMTDSALATLQPLHTLHSQLTQCTOLQTAE 140
CC -- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.				Qy 122 PRPRG-RLLHMLHLRQLQPKESAGCLEASFTNLFRLLTDLKVKVADGN 170
CC This Swiss-Prot entry is copyright. It is produced through a collaboration				Db 141 PKPPSRLSRSLWHLRQLQSKETPQPLHTLHSQLTQCTOLQTAE 190
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC the European Bioinformatics Institute. There are no restrictions on its				
CC use as long as its content is in no way modified and this statement is not				
CC removed.				
CC				
DR EMBL; AY129148; AN28263.1; - mRNA.				
DR EMBL; AY316715; AAR4510.1; - mRNA.				
DR Ensemble; ENSG00000163709; Homo sapiens.				
DR HGNC; HGNC:18364; IL28A.				
DR MIM: 607401; -				
KW Antiviral defense; Cytokine; Signal	1	25	Potential.	RESULT 5
FT SIGNAL	1	25		Q4VK73_MOUSE
FT CHAIN	26	200	Interleukin 28A.	ID Q4VK73_MOUSE PRELIMINARY;
FT CONFLICT	151	151	T > A (in Ref. 2).	AC Q4VK73;
SQ SEQUENCE	200 AA,	22288 MW;	DFC7B49P31BF488E CRC64;	DT 13-SEP-2005 (TREMBLrel. 31, Created)
				DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
				DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Interferon-lambda3.  
 GN Name=IL28; Synonyms=Ifnl3;  
 OS Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;  
 CC Muridae; Murine; Mus.  
 NCBI\_TaxID=10050;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 STRAIN=129/Sv;  
 RC PubMed=15914836; DOI=10.1099/vir.0.80904-0;  
 RX Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.; "Full house: 12 receptors for 27 cytokines.";  
 RA "Murine interferon lambda (type III interferons) exhibit potent  
 RT antiviral activity in vivo in a poxvirus infection model.";  
 RL J. Gen. Virol. 96:1589-1596 (2005).  
 DR EMBL: AAX38715.1; -; mRNA.  
 MGII: MGI:2450574; IL28.  
 SQ SEQUENCE 193 AA; 21690 MW; 9CBB2A23911F9B332 CRC64;  
 RT NUCLEOTIDE SEQUENCE.  
 STRAIN=129/Sv;  
 RC PubMed=15914836; DOI=10.1099/vir.0.80904-0;  
 RX Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.; "Full house: 12 receptors for 27 cytokines.";  
 RA "Murine interferon lambda (type III interferons) exhibit potent  
 RT antiviral activity in vivo in a poxvirus infection model.";  
 RL J. Gen. Virol. 96:1589-1596 (2005).  
 DR EMBL: AAX38715.1; -; mRNA.  
 MGII: MGI:2450574; IL28.  
 SQ SEQUENCE 193 AA; 21690 MW; 9CBB2A23911F9B332 CRC64;  
 Qy 3 PVP-TSKPTTNGKGCIGRKFLSISPOELASPKKARDALEESIQLKWNCSSPVFGNMDL 61  
 DB 21 PVPTRPLPVAKDCHIAQFSLSLSPKKAQKDAEKRLLDKYADGN 140  
 Qy 62 RLLQVERPVALAEALTLKVLEAAGPALEVDLQPLPLHLHLSQLOACIQOPTAG 121  
 DB 81 KQLOQVERPLAQAEVLTQWENINDSALTTLGQPLHTSHHSQLOCTQLOATAE 140  
 Qy 122 PRPRG-RLHWLHLRQEAQPKKESAGCLEASVTNFRLTRDLKYADGN 170  
 DB 141 PKPPSRRLSRWLHLRQEAQSKEPQCLEDSVTSNLFQLLRLDKCVASGD 190

RESULT 6  
 IL28 MOUSE STANDARD; PRT; 193 AA.  
 ID IL28\_MOUSE STANDARD; PRT; 193 AA.  
 AC Q8CGT6;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-SEP-2005 (Rel. 46, Last sequence update)  
 DE Interleukin 28 precursor (Interferon lambda) (IFN-lambda).  
 GN Name=IL28;  
 OS Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;  
 CC Muroidea; Muridae; Murine; Mus.  
 NCBI\_TaxID=10050;  
 RN NUCLEOTIDE SEQUENCE.  
 STRAIN=IC57BL/6;  
 RC PubMed=12483210; DOI=10.1038/ni875;  
 RA Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,  
 RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;  
 RT "IFN-lambda mediate antiviral protection through a distinct class II  
 CC cytokine receptor complex.";  
 RL Immunol. 4:69-77 (2003).  
 CC FUNCTION: Cytokine with immunomodulatory activity. May play a role  
 CC in antiviral immunity. Up-regulates MHC class I antigen  
 CC expression. Ligand for the heterodimeric class II cytokine  
 CC receptor composed of IL10RB and IL22RA. The ligand/receptor  
 CC complex seems to signal through the Jak-STAT pathway (By  
 CC similarity).  
 CC SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AY184375; AAC86128.1; -; mRNAs.  
 DR Ensembl; ENSMUSG00000066747; Mus musculus.  
 DR MGI; MGI:2450574; IL28.  
 KW Antiviral defense; Cytokine; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 193 Interleukin 28.  
 FT SEQUENCE 193 AA; 21664 MW; 357AA00AACABC61 CRC64;  
 CC Query Match 48.0%; Score 458; DB 1; Length 193;  
 CC Best Local Similarity 58.2%; Pred. No. 9.4e-34; Missmatches 50; Indels 2; Gaps 2;  
 CC Matches 99; Conservative 19; Signal 19; Signal 19; Potential 19;  
 CC SIGNAL 1 19  
 CC SEQUENCE 193 AA; 21664 MW; 357AA00AACABC61 CRC64;  
 Qy 3 PVP-TSKPTTNGKGCIGRKFLSISPOELASPKKARDALEESIQLKWNCSSPVFGNMDL 61  
 DB 21 PVPTRPLPVAKDCHIAQFSLSLSPKKAQKDAEKRLLDKYADGN 140  
 Qy 62 RLLQVERPVALAEALTLKVLEAAGPALEVDLQPLPLHLHLSQLOACIQOPTAG 121  
 DB 81 KQLOQVERPLAQAEVLTQWENINDSALTTLGQPLHTSHHSQLOCTQLOATAE 140  
 DB 122 PRPRG-RLHWLHLRQEAQPKKESAGCLEASVTNFRLTRDLKYADGN 170  
 Qy 122 PRPRG-RLHWLHLRQEAQPKKESAGCLEASVTNFRLTRDLKYADGN 170  
 DB 141 PKPPSRRLSRWLHLRQEAQSKEPQCLEDSVTSNLFQLLRLDKCVASGD 190  
 DB Name=ppk;  
 CC Acinetobacter baumannii; Gammaproteobacteria; Pseudomonadales;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonads;  
 CC Moraxellaceae; Acinetobacter.  
 OC Moraxellaceae; Acinetobacter.  
 NCBI\_TaxID=470;  
 RN [1]\_PPT\_ACIBA STANDARD; PRT; 692 AA.  
 ID \_PPT\_ACIBA  
 AC Q9XMB8;  
 AC MEDLINE=000507; PubMed=10527215;  
 AC "Regulation of polyphosphate kinase gene expression in Acinetobacter  
 CC baumannii 252.";  
 AC Microbiology 145:2931-2937(1999).  
 AC -!- FUNCTION: Catalyzes the reversible transfer of the terminal  
 CC phosphate of ATP to form a long-chain polyphosphate (polyP).  
 CC -!- CATALYTIC ACTIVITY: ATP + (phosphate)n = ADP + (phosphate)(n+1).  
 CC -!- PTM: An intermediate of this reaction is the autophosphorylated  
 CC ppk in which a phosphate is covalently linked to histidine  
 CC residues through a N-P bond (By similarity).  
 CC -!- SIMILARITY: Belongs to the polyphosphate kinase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AF116175; AAD28429.1; -; Genomic\_DNA.  
 DR HAMAP; MF\_00347; -; 1  
 DR InterPro; IPR0341; PP\_kinase.  
 DR Pfam; PF02503; PP\_kinase; 1.  
 DR

KW FT ACT_SITE 443	Phosphorylation; Transferase.	Phosphohistidine intermediate (By similarity).	Qy 108 SOLOACIQPQPTAGPRPRGLRHWWLHR-----LQEAKPKESAGCL-EASVTFN 154
PT FT ACT_SITE 462	Phosphohistidine intermediate (By similarity).	Db 481 MBKQAGRLDRPALAVMETSILPNWLDESEHTPDKLVLYGANRHODGNLQDYDLIT 540	
SQ SEQUENCE 692 AA;	78980 MW;	Score 97.5 ; DB 1; Length 692;	Qy 155 LFRLLTSDLK 164
Query Match	Best Local Similarity 22.6% ; Pred. No. 4..5;	Indels 53 ; Gaps 8;	Db 541 TYALPLRDL 550
Matches 42; Conservative 28; Mismatches 63; Gaps 8;			
Qy 24 LSPQELAS--FKKARDALEEESLKLKWNSCSPVFPGNWDLRLQVRERPVAL-----E 74	RESULT 9	Q8G5G0_BIFIO	
Db 85 LSPQEILHQSSETAHAALEHQYQILN---EQIPP-----QLRREGISFLRRGELTQ 132	ID Q8G5G0_BIFIO PRELIMINARY;	ID Q8G5G0_BIFIO PRELIMINARY;	PRT; 296 AA.
Qy 75 ABSLATKVLREAAAGPAEDVLDQPH-----TLHHILS-----OLQACIQPO 117	AC Q8G5G0;	AC Q8G5G0;	
Db 133 AQSNTWVKKYFQOQVAPALTPSPDPAHFPRLVNKSNIFVILEGDKAFGQDILAVVPA 192	DT 01-MAR-2003 (TREMBLrel. 23, Created)	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
Qy 118 PTAGPR-----PRGRLLHML-----HRLQEAKPKESAGCLEASVTENLFRLITRD 162	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
Db 193 PHSLPRVVRLPDDELTEKEHHVMLSSSTIHTAVSDSPFGMTATGCTQFRVTNADLTED 252	DE Hypothetical protein.	DE Hypothetical protein.	
Qy 163 LKYVAD 168	GN OrderdLocusNames=BL1052;	GN OrderdLocusNames=BL1052;	
Db 253 VEDLAE 258	OS Bifidobacterium longum.	OS Bifidobacterium longum.	
	OC Bacteriia; Actinobacteria; Actinobacteridae; Bifidobacteriales;	OC Bacteriia; Actinobacteria; Bifidobacterium.	
	OC Bifidobacteriaceae; Bifidobacterium.	OC Bifidobacteriaceae; Bifidobacterium.	
	RN [1] NCBI_TaxID=215816;	RN [1] NCBI_TaxID=215816;	
	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
	RC STRAIN=NCC 2705;	RC STRAIN=NCC 2705;	
	RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.2125227599;	RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.2125227599;	
	RA Schein M.A., Karmizantzu M., Snel B., Vilanova D., Berger B.,	RA Schein M.A., Karmizantzu M., Snel B., Vilanova D., Berger B.,	
	RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	
	RA Prindl R.D., Arigoni F.;	RA Prindl R.D., Arigoni F.;	
	RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract";	RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract";	
	RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).	RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).	
	DR EMBL; AE014295; AAC24858.1; -; Genomic DNA.	DR EMBL; AE014295; AAC24858.1; -; Genomic DNA.	
	KW Complete proteome; Hypothetical protein.	KW Complete proteome; Hypothetical protein.	
	SQ SEQUENCE 296 AA; 33881 MW; 54B29BC632765994E CRC64;	SQ SEQUENCE 296 AA; 33881 MW; 54B29BC632765994E CRC64;	
	Query Match 9.3%; Score 89 ; DB 2; Length 296;	Query Match 9.3%; Score 89 ; DB 2; Length 296;	
	Best Local Similarity 28.9%; Pred. No. 9.8;	Best Local Similarity 28.9%; Pred. No. 9.8;	
	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	
	Qy 46 KNW-SCSSPVFPGNWDLRL-LQVRERPVVAELALTKVLEAAGG-----PALEDVLD 97	Qy 46 KNW-SCSSPVFPGNWDLRL-LQVRERPVVAELALTKVLEAAGG-----PALEDVLD 97	
	Db 14 RTWRQCRTPAEPDQSVRQLTLLRGELETLLCVDAD 73	Db 14 RTWRQCRTPAEPDQSVRQLTLLRGELETLLCVDAD 73	
	Query Match 9.3%; Score 89 ; DB 2; Length 296;	Query Match 9.3%; Score 89 ; DB 2; Length 296;	
	Best Local Similarity 28.9%; Pred. No. 9.8;	Best Local Similarity 28.9%; Pred. No. 9.8;	
	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	
	Qy 98 QPLTFLHHLISQLCQCIQOPTAEPPRP-RGLHHLHLQEAQPKESAGCLEASVTFN 155	Qy 98 QPLTFLHHLISQLCQCIQOPTAEPPRP-RGLHHLHLQEAQPKESAGCLEASVTFN 155	
	Db 74 GPAQTLNRTRLKLTHPGVGR-TGAFLPRTGACHHLHLRKG-----IEHPLFEH 124	Db 74 GPAQTLNRTRLKLTHPGVGR-TGAFLPRTGACHHLHLRKG-----IEHPLFEH 124	
	Qy 156 PRLLTSDLKTVADGN 170	Qy 156 PRLLTSDLKTVADGN 170	
	Db 125 AR-NRD-RQVDDGD 136	Db 125 AR-NRD-RQVDDGD 136	
	RESULT 10	RESULT 10	
	Q8D6L0_SYNEL NUCLEOTIDE SEQUENCE.	Q8D6L0_SYNEL NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	RN 262 RLQYRERPVVAELALTKVLEAAGGPALED-VLDQPLHHLHHL 107	RN 262 RLQYRERPVVAELALTKVLEAAGGPALED-VLDQPLHHLHHL 107	
	Db 422 RLNIKDAVPSLPGCLNATLRPYOLEGSWMQSLRELEYGGVLAADDMGIGLKTLQTLAHL 480	Db 422 RLNIKDAVPSLPGCLNATLRPYOLEGSWMQSLRELEYGGVLAADDMGIGLKTLQTLAHL 480	
	Query Match 9.3%; Score 89 ; DB 2; Length 296;	Query Match 9.3%; Score 89 ; DB 2; Length 296;	
	Best Local Similarity 28.9%; Pred. No. 9.8;	Best Local Similarity 28.9%; Pred. No. 9.8;	
	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;	
	Qy 161 NUCLEOTIDE SEQUENCE.	Qy 161 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 162 NUCLEOTIDE SEQUENCE.	Qy 162 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 163 NUCLEOTIDE SEQUENCE.	Qy 163 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 164 NUCLEOTIDE SEQUENCE.	Qy 164 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 165 NUCLEOTIDE SEQUENCE.	Qy 165 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 166 NUCLEOTIDE SEQUENCE.	Qy 166 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 167 NUCLEOTIDE SEQUENCE.	Qy 167 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 168 NUCLEOTIDE SEQUENCE.	Qy 168 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 169 NUCLEOTIDE SEQUENCE.	Qy 169 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 170 NUCLEOTIDE SEQUENCE.	Qy 170 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 171 NUCLEOTIDE SEQUENCE.	Qy 171 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	
	DR GO:GO:0004386; F:halicase activity; IEA.	DR GO:GO:0004386; F:halicase activity; IEA.	
	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	RW SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	Query Match 9.4%; Score 89.5 ; DB 2; Length 914;	
	Best Local Similarity 26.2% ; Pred. No. 33;	Best Local Similarity 26.2% ; Pred. No. 33;	
	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;	
	Qy 172 NUCLEOTIDE SEQUENCE.	Qy 172 NUCLEOTIDE SEQUENCE.	
	RC Q8D6L0;	RC Q8D6L0;	
	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	RA Feil H., Peil W.S., Lindow S.E.; Submitted (MAY-2005) to the EMBL/GenBank/ DDBJ databases.	
	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	DR EMBL; CP000075; AAU36938.1; -; Genomic DNA.	



RA	Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.; "Draft sequence of the Giardia lamblia genome.", Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.	Query Match 9.1%; Best Local Similarity 25.6%; Pred. NO. 67; Mismatches 50; Conservative Matches 50; Gap 11;
RL	- ; CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
CC	DR AACB01000042; EAA40461.1; Genomic DNA.	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
DR	SEQUENCE 479 AA; 533677 MW; 70F50040A717818C CRC64;	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
SO	Query Match 9.1%; Best Local Similarity 25.6%; Pred. NO. 26; Mismatches 56; Indels 52; Gaps 7;	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
CC	SEQUENCE 479 AA; 533677 MW; 70F50040A717818C CRC64;	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
CC	Best Local Similarity 25.6%; Conservative Matches 23; Mismatches 56; Indels 52; Gaps 7;	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
DR	39 TSASKTIDKREKDLK---AYAKQQKAYEQ-MKQKQWSA-----	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
SO	71 VALEAELATLKVLEAAAGPAP- EDVLDQPLHTLHI----- ISLOQACIQPQ 117	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
DR	74 --EAENGQQLAVLKEARESILMKTMEQYHDLDDIWKTNKDSLDQAFLQSNLKG 130	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
SO	118 PTAGPRPRGRHLHHLRQEAQPKESACGSEASVTNFLFRLLTRDKVADGNLSL 173	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
DR	131 ATEKANRVSVLRDAKHLRHY-LKECSEGLLDRQ----- KDLDEHSIIAEALSL 175	Qy 14 KGCHIGRFKSLSPQELASPKKARDALEESLK --- LKNWCSSSPVPPGNWDLRLQYRE 68 Db 461 KGTEISSLSCNREAD---- LEEALRNRKTRALEEYTQNNEVRNGDHELA --- RE 510
SO	RESULT 14 Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
DR	10-MAY-2005 (TREMBLrel. 30, Last sequence update)	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
DR	10-MAY-2005 (TREMBLrel. 30, Last annotation update)	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
GN	ORFName=AN2756.2;	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
OS	Aspergillus nidulans FGSC A4.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericeillales; NCBI_TaxID=227321; [1]	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
RC	NUCLEOTIDE SEQUENCE.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
RC	STRAIN=FGSC A4;	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
RA	Birnboim C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky I., Bourgault B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K., Diaz J.S., Dodge S., Dooley K., Dooris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J., Gardyne S., Gneire S., Graham L., Grand-Pierre N., Hagopian D., Hago S., Hall J., Horron L., Huime W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Karatas A., Karpas A., Kellis C., Landers T., Levine R., Lindblad-Ton K., Liu A., Ma L.-J., Mabbitt R., MacLean C., McDonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Mihowa T., Mleking V., Murphy T., Naylor J., Nguyen C., Nicoli R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Rachapak A., Ranaibamy U., Raymond C., Recta R., Rose C., Ruse S., Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Testay S., Theodore J., Topham K., Travers M., Vasilev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.;	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
RT	"Sequence of Aspergillus nidulans"; "Genome Sequence of Aspergillus nidulans"; Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
RL	- ; CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
CC	DR AACD0100049; EAA63190.1; -; Genomic DNA.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
DR	Hypothetical protein.	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
SO	SEQUENCE 967 AA; 109021 MW; 9BC297B7E10A1159 CRC64;	Q5B9N4_EMENI_EMENI PRELIMINARY; PRT; 967 AA.
CC	Best Local Similarity 27.2%; Pred. NO. 21; Mismatches 53; Conservative Matches 18; Gap 10;	Qy 25 SPQELASPKKAR-DALEESLKLNWCSSSPVPPGNWDLR-- LLQYRERPVALEAL-AL 79 Db 81 SPEELATLVAELGPLESCLRV-----NPKSYGTWHHRCLWLSRLPEPNWARELCLCAR 134 Qy 80 TLKV-----LEAAAGSPALEVDLQPTLH-----HILSQLQACIQPQ 117

Db	135	FLEYDVERNFIWCWDYRFAAQQAVPAAELAFTDSLITRNFSNYSSWHRYSLLPQLHPQ	194
Qy	118	PTAGRPRGRRL-----	147
Db	195	PDSG--PQGRLPEDVLLKELEVQNAAFFDPNDQSAWFYHRWL-LGRADPQDALRCLHV	250
Qy	148	--EASVTNLFLRL 159	
Db	251	SRDAGCCTTYSFSPR 265	

Search completed: December 29, 2005, 13:59:11  
Job time : 230 secs

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OM protein - protein search, using SW model

Run on: December 29, 2005, 13:47:02 ; Search time 38 Seconds  
 (without alignments)  
 460.828 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPPPTSKPTTIGKCHIGR.....LKYVADGNLRLTSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : PIR 8.0:  
 1: Pir1:  
 2: Pir2:  
 3: Pir3:  
 4: Pir4:  
 \*:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	8.7	567	2 JC5538	Rab geranylgeranyl pre-mRNA splicing
2	82	8.6	899	2 S12319	hypothetical prote
3	81.5	8.5	530	2 C75318	HIV-1 retropepsin
4	81.5	8.5	553	1 B46335	probable aldehyde
5	81.5	8.5	1086	1 T35928	HIV-1 retropepsin
6	80.5	8.4	468	1 B46330	HIV-1 retropepsin
7	80.5	8.4	1101	1 GNLJVS	B1496_P2_81 prote
8	80.5	8.4	1101	1 S72782	Pol Protein - Maed
9	79.5	8.3	271	2 J01162	probable accD3 pro
10	79.5	8.3	1087	2 E70783	hypothetical prote
11	79	8.3	495	2 T24538	protein kinase (BC
12	79	8.3	557	2 AD0251	high-affinity zinc
13	78.5	8.2	253	1 A64686	protein kinase PKN
14	78.5	8.2	942	2 JC2129	hypothetical prote
15	77.5	8.1	217	2 H64186	hypothetical prote
16	77.5	8.1	371	2 E72665	protein kinase
17	77.5	8.1	946	2 JC2130	(BC
18	77	8.1	1035	2 A64686	cation efflux syst
19	77	8.1	775	2 T41961	hypothetical prote
20	77	8.1	3788	2 T13960	beige protein homo
21	76.5	8.0	1035	2 D71831	cation efflux syst
22	76	8.0	191	2 S57642	interferon precurs
23	76	8.0	528	2 CB3033	benzoylformate dec
24	75.5	7.9	403	2 S16603	hypothetical prote
25	75.5	7.9	559	2 AP3325	DNA repair protein
26	75.5	7.9	581	2 AF1923	hypothetical prote
27	75.5	7.9	649	2 J00103	hypothetical 70k p
28	75	7.9	654	2 I56134	tumor necrosis fac
29	75	7.9	640	1 S37869	probable serine/th

## ALIGNMENTS

RESULT 1  
 JC5538  
 Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human  
 C;Species: Homo sapiens (man)  
 C;Date: 01-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
 C;Accession: JC5538  
 R;Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.  
 Biochem. Biophys. Res. Commun. 235, 10-14, 1997  
 A;Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutaminase  
 A;Reference number: JC5538; MUID:97339427; PMID:9196026  
 A;Molecule type: DNA  
 A;Accession: JC5538  
 A;Residues: 1-567 <SON>  
 A;Cross-references: UNIPROT:092696; UNIPARC:UPI000013188E  
 C;Comment: This protein is involved in cutaneous disease.  
 C;Genetics:

A;Gene: Rabgta  
 A;Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 300/3; 336/2; 354/2; 383/2; 413  
 C;Keywords: transferase

Query Match Score 83; DB 2; Length 567;  
 Best Local Similarity 25.6%; Pred. No. 7.9;  
 Matches 50; Conservative 16; Mismatches 59; Indels 70; Gaps 9;

Qy 25 SPOELASFKEAR-DALEESULKRNNSCSPVPGNWDLRLQYRERPVV-LEAEALTLK 82  
 81 SPEELAALVTAELGLFLESCLRV-----NPKSYGTWHRCWLLGRLPENPNTRLELCAR 134  
 Qy 83 VLE-----ARAGPALEDVLDQDLHTLH-----HILSQLQACIQPQ 117  
 Db 135 FLEVDERNFICWDYTRRFVATQQAVVPAEELAFTDSLITRNFNSYYSWHYRSCLLQPQLHPQ 194  
 Qy 118 PTAGPRPRGRLL-----HHWLHLHQEAQPKESACGL-- 147  
 Db 195 PDSG----PQGRPLPEDVLLKELELVQNAFFTDNDQSAFWYHRWL-LGRADPQDARCLHV 250

RESULT 2  
 S12319  
 N;Alternate names: protein YR0508; protein YBR050C  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: S12319; S45913; S49510; S55854  
 R;Legrain, P.; Choulika, A.  
 EMBO J. 9, 2715-2781, 1990  
 A;Title: The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cyst  
 A;Reference number: S12319; MUID:9036088; PMID:2118103

A;Accession: S12319  
A;Molecule type: DNA  
A;Residues: 1-899 <LFG>  
A;Cross-references: UNIPROT:PI19735; UNIPARC:UPI00000530DB; EMBL:X53465; NID:94238; PID:NID:94238;  
R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
Submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45906  
A;Accession: S45913  
A;Molecule type: DNA  
A;Residues: 1-899 <ALJ>  
A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z35924; NID:9536290; PID:9536291; MIPS:Y  
A;Experimental source: strain S288C  
R;Aljinovic, G.  
Submitted to the EMBL Data Library, October 1994  
A;Description: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*  
A;Reference number: S49503  
A;Accession: S49510  
A;Molecule type: DNA  
A;Residues: 1-899 <AL2>  
A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z46260; NID:9559342; PID:9559951  
A;Experimental source: strain S288C  
R;Aljinovic, G.; Pohl, T.M.  
Year 11, 47-479, 1995  
A;Title: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*.  
A;Reference number: S55845; MUID:95321020; PMID:7597852  
A;Accession: S55854  
A>Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-899 <ALW>  
A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z46260; NID:9559942; PID:CAA86398.1; PI  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994  
C;Genetics:  
A;Gene: SGD:PRP6  
A;Cross-references: SGD:S0000259; MIPS:YBR055C  
A;Map position: 2R  
C;Keywords: nucleus; RNA binding; zinc finger

Query Match 8.6%; Score 82; DB 2; Length 899;  
Best Local Similarity 22.6%; Pred. No. 17;  
Matches 38; Conservative 27; Mismatches 61; Indels 42; Gaps 8;

Qy 33 RKKARDALESLKLKNWCSSSPVFPGNWDL-RILQVRR-----PVA 72  
Db 131 RNKRNRIQEQLNRTKIAAPDSLIPGNVNDLNKLTEERKLQSIDENLAQLTKNASNPQ 190

Qy 73 LEAELALT--IKVLEAAAGPALEVDIQLPLTHHILSLOQACIQOPTAGPRPRRLHH 130  
Db 191 VNKPNNAATDLSYLKDLDNRVNSLSATBDLQKRTILKSYRADPT---NPQG---- 243

Qy 131 WL-HRLQEAKPKESA -----GCLE---ASVTENFLFRLLTRDKY 165  
Db 244 WIASARLIEEKARKFSVAKKITENGQCPECPRSSDIWLENIRLHESDVHY 291

Matches 44; Conservative 19; Mismatches 68; Indels 25; Gaps 7;

Qy 25 SPQE-LASFYKKARDALEESTKLKNWCSSSPVFPGNWDLRL---LQVRERPVVALAEFLAL 79  
Db 6 SPSRLLRSRAGRFIAAPPVGFW-RSPGFGBGSIDARLALAHANARRAAALDINAM 63

Qy 80 TLKVLEAAAGPALEVDIQLPLHTLHHSLSL-QACIQOPTAGPRPRGRLLHHLRLQEA 138  
Db 64 -----AAGARLEAEVDEQORPUDQDVERVAEAVLVEETARARRAR----TAAEAA 111

Qy 139 PKKESEAGCLEASVTENFLFRLLTRDKYVADGNLSL 173  
Db 112 PEATAIAADEGRV----QIAKNDVALAYDANLSL 141

RESULT 4  
C75318 hypothetical protein - *Deinococcus radiodurans* (strain R1)  
C;Species: *Deinococcus radiodurans*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: C75318  
R;White, O.; Eisen, J.A.; Heddleberg, J.F.; Peterson, J.D.; Dodson, R.J.;  
M.; Shan, M.; Vahteran, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.  
S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.  
Science 266, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
A;Reference number: A75350; MUID:003696; PMID:10567166  
A;Accession: C75318  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-53 <WHI>  
A;Cross-references: UNIPROT:Q9RSN4; UNIPARC:UPI00000CIA67; GB:AE000513; NI:  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR2090  
A;Map position: 1

Query Match 8.5%; Score 81.5; DB 2; Length 553;  
Best Local Similarity 24.0%; Pred. No. 11;  
Matches 40; Conservative 16; Mismatches 64; Indels 47; Gaps 6;

Qy 3 PVPTSKPTTTRGKCHIGRFKSLSPDLSFKKARDALBEISLKLKNWCS-----S 52  
Db 125 PEPPKRPT-----KAAAPPAAASPEETTAAPASAPSGWLSSALNDWLKEPEA 174

Qy 53 PVFPGNWDLRLQVRERPVALEAHTLTKVLEAAGPA-----LFDVL-- 96  
Db 175 PAAPRREAAPARQVRSTATQTQ-----VIQAPKPKAPAPQPPSDPSLPLRTQELAS 228

Qy 97 -----DOPLHTLHHSLSLQACIQOPTAGPRPRGRLLHHLRLQEA 139  
Db 229 DRLPLPVELLERLVEQEQAA-QEQQEPAPAPAPVPRVVAALSSAP 274

RESULT 5  
B46315 HIV-1 retropeptain (EC 3.4.23.16) - Maedi/Vienna virus (strain SA-OMVV)  
N;Contains: endonuclease (EC 3.1.1.-); retropeptain (EC 3.4.23.16); RNA-directed DNA pol.  
C;Species: Maedi/Vienna virus  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 03-Jun-2002  
C;Accession: B46335  
R;Querat, G.; Audoly, G.; Sonigo, P.; Vigne, R.  
Virology 175, 434-447, 1990  
A;Title: Nucleotide sequence analysis of SA-OMVV, a viRNA-related ovine lentivirus: phylogenetic analysis  
A;Reference number: A46335; MUID:30223389; PMID:158181  
A;Accession: B46335  
A;Molecule type: DNA  
A;Residues: 1-1086 <QUE>  
A;Cross-references: UNIPARC:UPI0000131F0D; GB:M31646  
C;Comment: This protein is synthesized as a gag-pol polyprotein.  
C;Genetics:  
A;Gene: pol

Query Match 8.5%; Score 81.5; DB 2; Length 530;  
Best Local Similarity 28.4%; Pred. No. 10;

A;Accession: S52215 hypothetical protein 1 - rabies virus  
A;Species: rabies virus  
C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
C;Accession: S52215  
R;Camacho, A.; Tabaro, E.  
Submitted to the EMBL Data Library, June 1994  
A;Reference number: S52215  
A;Status: preliminary  
A;Molecule type: Genomic RNA  
A;Residues: 1-510 <CM>  
A;Cross-references: UNIPARC:UPI000017848C; EMBL:X79983  
A;Note: the source is designated as pseudorabies virus  
C;Superfamily: varicella-zoster virus gene 34 protein  
A;Gene: pol

C;Superfamily: poi polyprotein  
 C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleic acid polymerase #status predicted <REV>  
 P;20-120/Product: retropepsin #status predicted <REV>  
 P;129-841/Product: RNA-directed DNA Polymerase #status predicted <REV>  
 P;842-1086/Product: endonuclease #status predicted <ENC>  
 P;44/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.5%; Score 81.5; DB 1; Length 1086;  
 Best Local Similarity 30.0%; Pred. No. 23; Indels 15; Gaps 5;  
 Matches 27; Conservative 17; Mismatches 31; DB 1; Length 1086;

Qy 3 PVPTSKPTTGKCHIGRKFLSPLQELASFKKARDALEBESIKL--KWNSSCSPVF-- 55  
 Db 129 PIQVQLKEGCKGPHIAQ-PLTQEKLBSLKEIVDKEKEGVYGRAPPHTCNPICIK 187

Query Match 8.4%; Score 80.5; DB 1; Length 1101;  
 Best Local Similarity 31.6%; Pred. No. 30; Indels 15; Gaps 5;  
 Matches 25; Conservative 16; Mismatches 23; DB 1; Length 1101;

Qy 14 KGCHIGRFKSLSPQELASFKKARDALEBESIKL--KWNSSCSPVF---PGNW---D 60  
 Db 155 KGPFIAGW-PLTQEKGELKEVDRLEKEGVYGRAPPHTCNPICIKKKSGKWRMLID 213

RESULT 6

T35928 probable aldehyde dehydrogenase - Streptomyces coelicolor  
 C;Species: Streptomyces coelicolor  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T35928  
 R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, January 1999  
 A;Reference number: 221551  
 A;Accession: T35928  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-468 <SEB>  
 A;Cross-references: UNIPROT:Q9ZBH2; UNIPARC:UPI00000DAE91; EMBL:AL035206; PIDN:CAA22750.  
 A;Experimental source: strain A3(2)  
 C;Genetics:  
 A;Gene: SC9B5\_08  
 C;superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 8.4%; Score 80.5; DB 2; Length 468;  
 Best Local Similarity 25.7%; Pred. No. 11; Mismatches 16; DB 2; Length 468;

Matches 49; Conservative 16; Mismatches 75; Indels 51; Gaps 10;

Qy 1 MGPPVPTSKPTTGKCHIGRKFLSPLQELASFKKARDALEBESIKL-KWNSSCSPVF---- 54  
 Db 1 MAPATGPRHPTTORG---GYFAVVDPSGEAFEAEDPDRPEEL-----DPVDRARA 49

Qy 55 -FPGNWDRLQLQVRPVALEAELTLVLEAAA--GPALEDDVLDPLHTLHLILSQL 110  
 Db 50 AWG-W-----RADPAPRTALLAAMADAVERATAALAPLTTREQKPLTESHAEVART 101

Qy 111 QACIQ-----PQPTGPRPRGRHLRQLQEAPKESAGCLEASVTENFLFRLLTRD 162  
 Db 102 AARLYRFFAELDIAQPTTDPRVHSRLRW-----RSIGAVAATVPMN-FPLQIAS 150

Qy 163 LKV---VADGN 170  
 Db 151 AKFAPALLAGN 161

RESULT 7

HIV-1 retropepsin (EC 3.4.23.16) - Maedi/Visna virus (strain KV1772) (provirus)  
 N;Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA polymerase #status predicted <REV>  
 C;Species: Maedi/Visna virus  
 A;Note: host Homo sapiens (man)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
 C;Accession: B45390  
 R;Andresson, O.S.; Elmer, J.E.; Tobin, G.J.; Greenwood, J.D.; Gonda, M.A.; Georgeson, G.  
 J.W.; Pettersson, G.  
 Virology 199, 89-105, 1993  
 A;Title: Nucleotide sequence and biological properties of a pathogenic proviral molecule  
 A;Reference number: A45390; MUID:93174981; PMID:8384414.

submitted to the EMBL Data Library, November 1993  
A;Description: Mycobacterium leprae cosmid B1496.

submitted to the EMBL Data Library, November 1993  
A1.Description: Mycobacterium leprae Cosmid B1496.

A; Cross-references: UNIPROT:Q10561; UNIPARC:UPI0001251BA; GB:273101; GB:AL123456; NID  
A; Experimental source: strain H37RV

Sequence Comparison Details						
Query		Match		Statistics		
		Score	Length	DB	Mismatches	Gaps
Best	Local	8.3%	271	DB 2;	Length 271;	
Accession:	S72782					
Status:	Preliminary					
Molecule type:	DNA					
Residues:	1-271 <SMI>					
Cross-references:	UNIPROT:Q49706; UNIPARC:UPI00000D4381; EMBL:U00013; NID:g466868; PID:					
36	RDALEESKLKNWISCSSPVPFG--NW-DILRLQ-VRERPVALAELALTKVLEA-AAG	89				
69	RICATELSLKVR---SAPAMNGKFDWLDSKXVQVMVPDWPEHSTIAUTGVNLSNTNFKTG	124				
90	PALEDDVLDOPLTLHHISLQLQACIQOPTAGPPRGRHLHWHLRQEAPKRESAGCLEA	149				
125	PATLGIAIDSNHTFTVTIDGVEA-ETPPLPLSP-----HHRPHWGEGVMPASMGKTEF	177				
150	SVTFLNFRFLLTDRDKYVADGN	170				
178	PTPTGKCTVMSKDRSVMDSS	198				

		Best Local Similarity	Best Local Matches	Pred.	No.	Mismatches	Indels	Gaps	5;
Y	Y	31.68	25;	Conservative	16;	KNWSSCPVF---PGNW---D	60		
Y	Y	14	KGCHIGRFKSLSPQELASFKKARDALESSLKL--	--					
b	b	139	KPHIAQW-PLTOBKLEGIEKEYVRLEREGKLGRAAPPWWTCNTPIFCIKKKSSKWRMID	197					
Y	Y	61	LRLLQVRPVALAEELAL	79					
b	b	198	FRELINKQFEDLA-BAQGL	215					

RESULT 11  
 E70783 |Unprobable accD3 protein - Mycobacterium tuberculosis (strain H37RV)  
 /Species: Mycobacterium tuberculosis  
 /Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 /Accession: E70783  
 /Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 /Reference number: A70500;  
 /Accession: E70783  
 /Status: preliminary; nucleic acid sequence not shown; translation not shown  
 /Molecule type: DNA  
 /Residue: 1-495 <COL>

A; Cross-references: UNIPROT:Q10561; UNIPARC:UPI0001251BA; GB:273101; GB:AL123456; NID  
A; Experimental source: strain H37RV

Sequence Comparison Details						
Query		Match		Statistics		
		Score	Length	DB	Mismatches	Gaps
Best Local Matches	8.37%	Score: 79.5	Length: 271			
Local Similarity	26.28%	DB: 2				
Residues	24	Prod. No.: 6.9				
Cross-references	1-271	Mismatches: 63				
Accession	S72782	Indels: 17				
Status	Preliminary	Gaps: 7				
Molecule type	DNA					
Residues	<SMI>					
UniProt ID	Q49706					
UNIPARC ID	UPI00000D4381					
EMBL ID	U00013					
NID	g466868					
PI						

		Best Local Similarity	Best Local Matches	Pred.	No.	Mismatches	Indels	Gaps	5;
Y	Y	31.68	25;	Conservative	16;	KNWSSCPVF---PGNW---D	60		
Y	Y	14	KGCHIGRFKSLSPQELASFKKARDALESSLKL--	--					
b	b	139	KPHIAQW-PLTOBKLEGIEKEYVRLEREGKLGRAAPPWWTCNTPIFCIKKKSSKWRMID	197					
Y	Y	61	LRLLQVRPVALAEELAL	79					
b	b	198	FRELINKQFEDLA-BAQGL	215					

RESULT 11  
 E70783 |Unprobable accD3 protein - Mycobacterium tuberculosis (strain H37RV)  
 /Species: Mycobacterium tuberculosis  
 /Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 /Accession: E70783  
 /Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 /Reference number: A70500;  
 /Accession: E70783  
 /Status: preliminary; nucleic acid sequence not shown; translation not shown  
 /Molecule type: DNA  
 /Residue: 1-495 <COL>

A; Accession: AD0251 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-253 <KUR> A; Cross-references: UNIPROT:Q8ZEU3 ; UNIPARC:UPI00000DC6DD ; GB AL590842 ; PIDN: CAC90872.1; C; Genetics: A; Gene: znuC	Query Match 8.2% ; Score 78.5; DB 2; Length 253; Best Local Similarity 28.1%; Pred. No. 7.9; Matches 45; Conservative 21; Mismatches 47; Indels 47; Gaps 9;	Qy 48 WSCSPVPGNMDLRLQVRERPVALFELALW-----TLKVLLEAAGPALEDVLDQ 98 Db 407 W---KPCGPNAHQSPFLBLER-ARELELAIVFDORGICLAKFLK-----LBDFLDN 455
		Qy 99 PLHTLHILSQLOACIQPQTAGPRPRGRLLHWHLRLOEAPKESAGCLEASVTF 153 Db 456 ERH-----EVQDMBPQ-----GCLVAEVTF 476
	RESULT 15 H64186	
		hypothetical protein HII159 - Haemophilus influenzae (strain Rd KW20) Species: Haemophilus influenzae C; Date: 18-Aug-1995 #sequence_change 18-Aug-1995 #text_change 09-Jul-2004 C; Accession: H64186 R; Fiebschmann, M.D.; Adams, R.D.; Kirkness, E.B.; Kerlavage, R.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995 A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000 ; MUID:95150630 ; PMID:752800 A; Accession: H64186 A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-217 <TIGR> A; Cross-references: UNIPARC:UPI000013A2D0 ; GB:U32795 ; GB:L42023 ; NID:91
		Query Match 8.1% ; Score 77.5; DB 2; Length 217; Best Local Similarity 26.2%; Pred. No. 8.2; Mismatches 26; Indels 35; Gaps 9; Matches 45; Conservative 26; Mismatches 66;
		Qy 9 PTTGKGCHIGFKLSP-QELASFKKARDALFEESLKLKNWCSSPVPGNMDLRLQYR 67 Db 27 PSVLDKSSLIQNLISIUPKEEDLFQQLADFLQ----VENYRRAPLLKDWFLS--DKK 80
	RESULT 16 JC2129	
		ERPV-AEABLLTLYLEAAGPALEDVLDQ-PLTLLHILSQLQRCIQOPTAGPPR 125 Qy 68 ERPV-AEABLLTLYLEAAGPALEDVLDQ-PLTLLHILSQLQRCIQOPTAGPPR 125 Db 81 NSDVALLYAETTYAMKKTEPA---QEILNQIPLQDRDSRMHGLQAOIELQQAADTP 135
		Qy 126 GRLLHHWLRLOE-----APKESAGCLEASVTFNLFRLITRDL 163 Db 136 -----IQQLQADYAKNPTAEIAKLVQHLQARGNEBEATL-LFGILKTDL 180
	Search completed: December 29, 2005, 13:59:53 Job time : 40 secs	
		A; Residues: 1-942 <MDR> A; Cross-references: UNIPROT:Q16512 ; UNIPARC:UPI000013CB15 ; GB:D26181 ; PIDN: 9473712; R; Palmer, R.H.; Ridder, J.; Parker, P.J. Bur. J. Biochem. 227, 344-351, 1995 A; Title: Cloning and expression patterns of two members of a novel protein-kinase-C-related A; Reference number: 153327 ; MUID:94183274 ; PMID:813837 A; Accession: S67526 A; Molecule type: mRNA A; Residues: 1-190, 'D'-192-942 <PAL> A; Cross-references: UNIPARC:UPI0000131B6B ; EMBL:S75546 ; PIDN:9514097 ; PIDN:AAB33345.1; PI A; Experimental source: fetal brain R; Palmer, R.H.; Ridder, J.; Parker, P.J. PEBS Lett. 356, 5-8, 1994 A; Title: Identification of multiple, novel, protein kinase C-related gene products. A; Reference number: 551020 ; MUID:95080426 ; PMID:7988719 A; Accession: S51020 A; Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra A; Molecule type: mRNA A; Residues: 700-799, 'A' <PA2> A; Cross-references: UNIPARC:UPI000017A3BB C; Comment: This protein has a protein kinase domain related to protein kinase C. C; Keywords: ATP; leucine zipper; phosphotransferase, protein kinase F; 39-56/Region: basic F; 70-87/Region: leucine zipper motif F; 613-874/Region: leucine zipper motif F; 621-629/Region: protein kinase ATP-binding motif F; 644/Active site: Lys #status predicted
		Query Match 8.2% ; Score 78.5; DB 2; Length 942; Best Local Similarity 28.6%; Pred. No. 38; Mismatches 40; Indels 71; Gaps 13; Matches 50; Conservative 14; Mismatches 40; Indels 71; Gaps 13;
	Qy 2 GP-VPTSKP----TTTGKGCHIGFKLSPQELASFKKARDALFEESLKLKN-----47 Db 350 GPCTPDSPRPFSLSPARGLY-SRSGSLSGR--SSLKAEAENTSEVSTVLKLKDNTVVGOTS 406	



This sequence represents a mutant interleukin IL-28A, Met-C172S. This interleukin protein may be used in the method of the invention for treating a viral infection. The method comprises administering to a mammal with a viral infection causing liver inflammation, an interleukin-based polypeptide, where the viral infection level or liver inflammation is reduced. The reduction in the viral infection level is measured as a decrease in viral load, an increase in anti-viral antibodies, a decrease in serological levels of alanine aminotransferase or histological improvement. The viral infection is hepatitis B or C virus infection. The mammal has cytopenia, comprising leukocyte deficiency, neutropenia, thrombocytopenia or anaemia. The interleukin polypeptide is interleukin 28 or 29, or a variant of these. The method of the invention is useful in treating hepatitis B or C virus infection.

XX Sequence 182 AA;

Query Match Score 955; DB 8; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.8e-91;  
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SQ 1 MGPPVPTSKPPTNGKGCHIGRFKSLSPOLASKARDALEESLKLXNWCSSPVFFGNWD 60  
Db 1 MGPPVPTSKPPTNGKGCHIGRFKSLSPOLASKARDALEESLKLXNWCSSPVFFGNWD 60  
Qy 1 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Db 1 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Qy 121 GPRPRGLHHWHLRQLQAPKKESSAGCLEASVTNFLFRLTRDLYVADGNLSLRSTHPE 180  
Db 121 GPRPRGLHHWHLRQLQAPKKESSAGCLEASVTNFLFRLTRDLYVADGNLSLRSTHPE 180  
Qy 181 ST 182  
Db 181 ST 182

RESULT 2  
ADY03602  
ID ADY03602 standard; protein; 182 AA.

XX ADY03602;

XX 05-MAY-2005 (first entry)

DE Human IL-29 mutant protein sequence SeqID29.  
KW antiviral; pharmaceutical; hepatitis b virus infection;  
KW hepatitis c virus infection; mutant; mutein; IL-29.  
OS Homo sapiens.  
OS Synthetic.  
PN US2005037012-A1.  
PD 17-FEB-2005.

XX PF 09-AUG-2004; 2004US-00914772.  
PR 07-AUG-2003; 2003US-0493194P.  
PR 10-MAR-2004; 2004US-055181P.  
PR 02-APR-2004; 2004US-0559142P.  
XX (BRAD/) BRADY L J.  
PA (KLUCH/) KLUCHEK K M.  
PA (CHAN/) CHAN C.  
PA (DONG/) DONG D L.  
PA (LIUH/) LIU H Y.  
PA (SHEP/) SHEPPARD P O.  
PA (BUKOK/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO; PI Bukowski TR;

XX WPI; 2005-180368/19.  
DR N-PDB; ADY03601.  
XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.  
XX PS Claim 1; SEQ ID NO 29; 149pp; English.  
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.  
XX SQ Sequence 182 AA;  
Query Match Score 955; DB 9; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.8e-91;  
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGPPVPTSKPPTNGKGCHIGRFKSLSPOLASKARDALEESLKLXNWCSSPVFFGNWD 60  
Db 1 MGPPVPTSKPPTNGKGCHIGRFKSLSPOLASKARDALEESLKLXNWCSSPVFFGNWD 60  
Qy 1 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Db 1 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Qy 61 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Db 61 LRLLQYRERPVALEELATKVLEAAAGPALEDVLDQPLTHLHILSOLACIQOPTA 120  
Qy 121 GPRPRGLHHWHLRQLQAPKKESSAGCLEASVTNFLFRLTRDLYVADGNLSLRSTHPE 180  
Db 121 GPRPRGLHHWHLRQLQAPKKESSAGCLEASVTNFLFRLTRDLYVADGNLSLRSTHPE 180  
Qy 181 ST 182  
Db 181 ST 182  
Db 181 ST 182

RESULT 3  
ADY03614  
ID ADY03614 standard; protein; 182 AA.  
XX ADY03614;  
AC ADY03614;  
XX 05-MAY-2005 (first entry)  
DT XX Human IL-28A mutant protein sequence SeqID41.  
DE XX antiviral; pharmaceutical; hepatitis b virus infection;  
KW XX hepatitis c virus infection; mutant; mutein; IL-28A.  
OS XX Homo sapiens.  
OS Synthetic.  
OS XX US2005037012-A1.  
PN XX 17-FEB-2005.  
PR XX 09-AUG-2004; 2004US-00914772.  
PR XX 07-AUG-2003; 2003US-0493194P.  
PR XX 10-MAR-2004; 2004US-055181P.  
PR XX 02-APR-2004; 2004US-0559142P.  
XX PR 07-AUG-2003; 2003US-0493194P.  
PR XX 10-MAR-2004; 2004US-0551841P.  
PR XX 02-APR-2004; 2004US-0559142P.  
PA PA (BRAD/) BRADY L J.  
PA PA (KLUCH/) KLUCHEK K M.  
PA PA (CHAN/) CHAN C.  
PA PA (DONG/) DONG D L.  
PA PA (LIUH/) LIU H Y.  
PA PA (SHEP/) SHEPPARD P O.  
PA PA (BUKOK/) BUKOWSKI T R.

xx Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO; PR 18-APR-2003; 2003US-0463939P.  
 PI Bukowski TR; PR 18-APR-2003; 2003US-0463982P.  
 PI XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 DR WPI; 2005-180368/19. XX  
 DR N-PSDB; ADY03608. XX  
 XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti- PT  
 PT viral activity, useful for treating hepatitis B or hepatitis C PR  
 PT infections. XX  
 PS Claim 1: SEQ ID NO 41; 149pp; English.  
 XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.  
 XX Sequence 182 AA:  
 Query Match 99.6%; Score 951; DB 9; Length 182;  
 Best Local Similarity 99.5%; Pred. No. 7.3e-91;  
 Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MGPPVPTSKPTTGGKGCHIGRFKSLSPQLASPKKKARDALLESILKIKWNWSCSSSPVFGNWD 60  
 Db 1 MGPPVPTSKPTTGGKGCHIGRFKSLSPQLASPKKKARDALLESILKIKWNWSCSSSPVFGNWD 60  
 Qy 61 LRLQVRERPVVALEALATLKVLEAGPALEDVLQPLTHLHHLISQLACIQOPTA 120  
 Db 61 LRLQVRERPVVALEALATLKVLEAGPALEDVLQPLTHLHHLISQLACIQOPTA 120  
 Qy 121 GPRPRGRHHWHLRQEAPKESAGCLEASITFNLFULTRDLYVADGNLSLRSTHPE 180  
 Db 121 GPRPRGRHHWHLRQEAPKESAGCLEASITFNLFULTRDLYVADGNLXLRSTHPE 180  
 Qy 181 ST 182  
 Db 181 ST 182  
 RESULT 4  
 AD059972 ID AD059972 standard; protein; 181 AA.  
 AC AD059972;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE IL-28A mutant C171S.  
 XX KW interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;  
 KW viral load; anti-viral antibody; serological level;  
 KW alanine aminotransferase; histological improvement; hepatitis B;  
 KW hepatitis C; cytopaenia; leucocyte deficiency; neutropenia;  
 KW thrombocytopenia; anaemia; IL-29.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FT Misc-difference 171 /label= C171S  
 FN WO2004037995-A2.  
 PD 06-MAY-2004.  
 XX PP 23-OCT-2003; 2003WO-US033658.  
 PN XX PR 23-OCT-2002; 2002US-0420713P.  
 PR 23-OCT-2002; 2002US-0420714P.  
 PR 2004-365507/34.  
 PR N-PSDB; ADY05971.  
 XX DR 2004-365507/34.  
 XX PR 18-APR-2003; 2003US-0463982P.  
 XX PA XX  
 PI Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KB;  
 XX WPI; 2004-365507/34.  
 XX DR N-PSDB; ADY05971.  
 XX PR 18-APR-2003; 2003US-0463939P.  
 XX PA XX  
 PT Treating hepatitis B or hepatitis C virus infection comprises  
 PT administering to a mammal with a viral infection causing liver  
 PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide  
 PT group.  
 XX Claim 12; SEQ ID NO 32; 102pp; English.  
 XX This sequence represents a mutant interleukin IL-28A, Met-C171S. This interleukin protein may be used in the method of the invention for  
 CC treating a viral infection causing liver inflammation, an interleukin-  
 CC based polypeptide, where the viral infection level or liver inflammation  
 CC is reduced. The reduction in the viral infection level is measured as a  
 CC decrease in viral load, an increase in anti-viral antibodies, a decrease  
 CC in serological levels of alanine aminotransferase or histological  
 CC improvement. The viral infection is hepatitis B or C virus infection. The  
 CC mammal has cytopenia, comprising leukocyte deficiency, neutropenia,  
 CC thrombocytopenia or anaemia. The interleukin polypeptide is interleukin  
 CC 28 or 29, or a variant of these. The method of the invention is useful in  
 CC treating hepatitis B or C virus infection.  
 XX Sequence 181 AA:  
 Query Match 99.5%; Score 950; DB 8; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-91;  
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 GPVPTSKPTTGGKGCHIGRFKSLSPQLASPKKKARDALLESILKIKWNWSCSSSPVFGNWD 61  
 Db 1 GPVPTSKPTTGGKGCHIGRFKSLSPQLASPKKKARDALLESILKIKWNWSCSSSPVFGNWD 60  
 Qy 62 RLLQVRERPVVALEALATLKVLEAGPALEDVLQPLTHLHHLISQLACIQOPTAG 121  
 Db 61 RLLQVRERPVVALEALATLKVLEAGPALEDVLQPLTHLHHLISQLACIQOPTAG 120  
 Qy 122 PRPRGRHHWHLRQEAPKESAGCLEASITFNLFULTRDLYVADGNLSLRSTHPE 181  
 Db 121 PRPRGRHHWHLRQEAPKESAGCLEASITFNLFULTRDLYVADGNLXLRSTHPE 180  
 Qy 182 T 182  
 Db 181 T 181  
 RESULT 5  
 ADY03600 ID ADY03600 standard; protein; 181 AA.  
 AC ADY03600;  
 XX DT 05-MAY-2005 (first entry)  
 XX DE Human IL-29 mutant protein sequence SeqID27.  
 XX KW antiviral; pharmaceutical; hepatitis b virus infection;  
 KW hepatitis c virus infection; mutant; murine; IL-29.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PR 2005037012-A1.  
 PN XX US2005037012-A1.  
 PR XX PD 17-FEB-2005.



XX	antiviral; pharmaceutical; hepatitis b virus infection;	DT 05-MAY-2005 (first entry)
KW	hepatitis c virus infection; mutant; mutein; IL-29.	XX Human IL-29 mutant protein sequence SeqID151.
XX	Homo sapiens.	XX
OS	Synthetic.	KW antiviral; pharmaceutical; hepatitis b virus infection;
OS		KW hepatitis c virus infection; mutant; mutein; IL-29.
XX		XX
PN	US2005037012-A1.	OS Homo sapiens.
XX		Synthetic.
PD	17-FEB-2005.	XX
XX		US2005037012-A1.
PP	09-AUG-2004; 2004US-00914772.	XX
XX		PD 17-FEB-2005.
PR	07-AUG-2003; 2004US-0493194P.	XX
PR	10-MAR-2004; 2004US-051841P.	PP 09-AUG-2004; 2004US-00914772.
PR	02-APR-2004; 2004US-0559142P.	XX
XX		XX 07-AUG-2003; 2003US-0493194P.
PA	(BRAD/) BRADY L J.	PR 10-MAR-2004; 2004US-051841P.
PA	(KLUC/) KLUCHER K M.	PR 02-APR-2004; 2004US-0559142P.
PA	(CHAN/) CHAN C.	XX
PA	(DONG/) DONG D L.	(BRAD/) BRADY L J.
PA	(LIUH/) LIU H Y.	PA (KLUC/) KLUCHER K M.
PA	(SHEPPARD) SHEPPARD P O.	PA (CHAN/) CHAN C.
PA	(BUKO/) BUKOWSKI T R.	PA (DONG/) DONG D L.
PI	Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;	PA (LIUH/) LIU H Y.
PI	Bukowski TR;	PA (SHEPPARD) SHEPPARD P O.
XX		PA (BUKO/) BUKOWSKI T R.
DR	WPI; 2005-180368/19.	XX
DR	N-PSDB; ADY03587.	DR PI
XX		PT DR N-PSDB; ADY0373.
PT	Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C	XX
PT	Example 19; SEQ ID NO 15; 149pp; English.	PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C
XX		PT PT viral activity, useful for treating hepatitis B or hepatitis C
CC	This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.	XX PS Claim 1; SEQ ID NO 151; 149pp; English.
CC		XX CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.
CC		XX CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.
SQ	Sequence 182 AA;	XX SQ Sequence 183 AA;
Query Match	99.5%; Score 950; DB 9; Length 182;	XX SQ Sequence 183 AA;
Best Local Similarity	99.5%; Pred. No. 9_3e-91;	Query Match 99.3%; Score 948; DB 9; Length 183;
Matches	181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Best Local Similarity 98.9%; Pred. No. 1.5e-90;
Qy	1 MGIVPVTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 60	Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db	1 MGIVPVTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 60	Qy 1 MGIVPVTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 60
Qy	61 LRLLQVRPVALEALTLKVLEAAGPALEDVLDQPLTHLILQLQACIQOPTA 120	Db 2 LGPVPTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 61
Db	61 LRLLQVRPVALEALTLKVLEAAGPALEDVLDQPLTHLILQLQACIQOPTA 120	Qy 61 LRLLQVRPVALEALTLKVLEAAGPALEDVLDQPLTHLILQLQACIQOPTA 120
Qy	61 LRLLQVRPVALEALTLKVLEAAGPALEDVLDQPLTHLILQLQACIQOPTA 120	Db 62 LGPVPTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 61
Db	121 GPPRGRHLHHWLQEPKKESSAGCLEASVTFNLFRLLTRDLKYVADGNLSLRSTHPE 180	Qy 62 LGPVPTISKPTTIGKGGCHIGRFKSLSPQLASFKKARDALEEESLKLKNWCSSSPVFPGNWD 61
Qy	121 GPPRGRHLHHWLQEPKKESSAGCLEASVTFNLFRLLTRDLKYVADGNLSLRSTHPE 180	Db 121 GPPRGRHLHHWLQEPKKESSAGCLEASVTFNLFRLLTRDLKYVADGNLSLRSTHPE 180
Db	181 ST 182	Qy 121 GPPRGRHLHHWLQEPKKESSAGCLEASVTFNLFRLLTRDLKYVADGNLSLRSTHPE 180
Db	181 ST 182	Db 122 GPPRGRHLHHWLQEPKKESSAGCLEASVTFNLFRLLTRDLKYVADGNLSLRSTHPE 181
RESULT 8		Qy 181 ST 182
ADY03724		Db 182 ST 183
ID ADY03724 standard; protein; 183 AA.		
XX		
AC ADY03724		
XX		
RESULT 9		
ADY03728		
ID ADY03728 standard; protein; 183 AA.		
XX		
AC ADY03728		
XX		

XX	AC ADY03728;	RESULT 10
XX	DT 05-MAY-2005 (first entry)	ID ADY03613 standard; protein; 181 AA.
XX	DE Human IL-29 mutant protein sequence SeqID155.	ID ADY03613;
XX	KW antiviral; pharmaceutical; hepatitis b virus infection; hepatitis c virus infection; mutant; mutein; IL-29.	AC ADY03613;
XX	OS Homo sapiens.	XX
XX	Synthetic.	XX
OS		XX
XX	PNI US2005037012-A1.	XX
XX	PD 17-FEB-2005.	PN US2005037012-A1.
PF 09-AUG-2004; 2004US-00914772.	XX	XX
XX	PR 07-AUG-2003; 2003US-0493194P.	PD 17-FEB-2005.
PR 10-MAR-2004; 2004US-0551841P.	XX	XX
PR 02-APR-2004; 2004US-0559142P.	XX	PP 09-AUG-2004; 2004US-00914772.
XX	(BRAD/) BRADY L J.	XX
PA (KLUC/) KLUCHER K M.	XX	PR 07-AUG-2003; 2003US-0493194P.
PA (CHAN/) CHAN C.	XX	PR 10-MAR-2004; 2004US-0551841P.
PA (DONG/) DONG D L.	XX	PR 02-APR-2004; 2004US-0559142P.
PA (LIUH/) LIU H Y.	XX	(BRAD/) BRADY L J.
PA (SHEP/) SHEPPARD P O.	XX	PA (KLUC/) KLUCHER K M.
PA (BURKO/) BUKOWSKI T R.	XX	PA (CBRN/) CHAN C.
PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO; Bukowski TR;	XX	PA (DONG/) DONG D L.
XX	WPI; 2005-180368/19.	PA (LITCH/) LIU H Y.
XX	N-PSDB; ADY03727.	PA (SHEP/) SHEPPARD P O.
XX	Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.	PA (BUKO/) BUKOWSKI T R.
XX	Claim 1; SEQ ID NO 155; 149pp; English.	XX
XX	This invention relates to novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.	PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.
XX	Sequence 183 AA;	PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.
XX	Query Match 99.2%; Score 947; DB 9; Length 183;	XX
XX	Best Local Similarity 98.3%; Pred. No. 1.9e-90; 1; Indels 0; Gaps 0;	PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.
XX	Matches 180; Conservative 1; Mismatches 1; Gaps 0;	XX
Qy 1 MGPPVPTSKPTTGKCHIGRKFKSLSPQELASFKKKARDALLESLKLKNWCSSPVPGNWLD 60	Query Match 99.1%; Score 946; DB 9; Length 181;	XX
Db 2 IGPVPTSKPTTGKCHIGRKFKSLSPQELASFKKKARDALLESLKLKNWCSSPVPGNWLD 61	Best Local Similarity 99.4%; Pred. No. 2.4e-90; 0; Mismatches 0; Indels 0; Gaps 0;	XX
Qy 61 LRLQQYRERPVALEELAATLKVLEAAAGPALEVDQLPLHTLHILSLOACIQPQTA 120	Qy 2 GPVPSSKPTTGKCHIGRKFKSLSPQELASFKKKARDALLESLKLKNWCSSPVPGNWLD 61	XX
Db 62 LRLQQYRERPVALEELAATLKVLEAAAGPALEVDQLPLHTLHILSLOACIQPQTA 121	Db 1 GPVPSSKPTTGKCHIGRKFKSLSPQELASFKKKARDALLESLKLKNWCSSPVPGNWLD 60	XX
Qy 121 GPRPRGLHHWLRHQEPKKEASGGLEEASVTENFLRDLKYVADGNLSLRSTHPE 180	Qy 62 RLQQYRERPVALEELAATLKVLEAAAGPALEVDQLPLHTLHILSLOACIQPQTA 121	XX
Db 122 GPRPRGLHHWLRHQEPKKEASGGLEEASVTENFLRDLKYVADGNLSLRSTHPE 181	Db 61 RLQQYRERPVALEELAATLKVLEAAAGPALEVDQLPLHTLHILSLOACIQPQTA 120	XX
Qy 181 ST 182	Qy 122 PRPRGLHHWLRHQEPKKEASGGLEEASVTENFLRDLKYVADGNLSLRSTHPE 181	XX
Db 182 ST 183	Db 121 PRPRGLHHWLRHQEPKKEASGGLEEASVTENFLRDLKYVADGNLSLRSTHPE 180	XX

Db	181 T 181	Qy	181 ST 182
<b>RESULT 11</b>			
ID ADY03658	standard; protein; 182 AA.	Db	181 ST 182
XX AC ADY03658;			
XX DT 05-MAY-2005 (first entry)			
XX DE Human IL-29 mutant protein sequence SeqID85.			
XX KW antiviral; pharmaceutical; hepatitis b virus infection;			
XX KW hepatitis c virus infection; mutant; mutein; IL-29.			
XX OS Homo sapiens.			
XX OS Synthetic.			
PN US2005037012-A1.			
XX PD 17-FEB-2005.			
XX PP 09-AUG-2004; 2004US-00914772.			
PR 07-AUG-2003; 2003US-0493194P.			
PR 10-MAR-2004; 2004US-0551841P.			
PR 02-APR-2004; 2004US-0559142P.			
XX PA (BRAD/) BRADY L J.			
PA (KLUC/) KLUCHER K M.			
PA (CHAN/) CHAN C.			
PA (DONG/) DONG D L.			
PA (LIU/) LIU H Y.			
PA (SHEPP/) SHEPPARD P O.			
PA (BUKO/) BUKOWSKI T R.			
PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;			
PI Bukowski TR;			
XX WPI: 2005-180368/19.			
DR N-PSDB; ADY03657.			
XX PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.			
PT PS Claim 1; SEQ ID NO 85; 149pp; English.			
CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.			
XX SQ Sequence 182 AA;			
Query Match 1 MGIVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Score 946; DB 9; Length 182;	Best Local Similarity 99.1%; Score 946; DB 9; Length 185;	
Best Local Similarity 98.9%; Pred. No. 2.4e-90; Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy 1 MGIVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Qy 2 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Qy 2 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Qy 2 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND 61
Db 1 MGIVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Db 5 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Db 5 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Db 5 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND 64
Qy 61 LRLQVRERPVALEELATLKVLAAAGPALEVDLDQPLTLHHLSQLQACIQOPTA 120	Qy 62 RLLQVRERPVALEELATLKVLAAAGPALEVDLDQPLTLHHLSQLQACIQOPTA 121	Qy 62 RLLQVRERPVALEELATLKVLAAAGPALEVDLDQPLTLHHLSQLQACIQOPTA 121	Qy 62 RLLQVRERPVALEELATLKVLAAAGPALEVDLDQPLTLHHLSQLQACIQOPTA 121
Db 61 LRLQVRERPVALEELATLKVLAAAGPALEVDLDQPLTLHHLSQLQACIQOPTA 120	Db 65 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Db 65 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND	Db 65 GPVPFSKPTTGKCHIGREKFLSPOELASFKKKARDALLESLKLKWNSCSSSPVPGNND
Qy 121 GPRPRGRLLHHLQLQAEPKKESAGCLESYTTFNLRLTRDLKYADGNLSLRSTTHPE 180			
Db 121 GPRPRGRLLHHLQLQAEPKKESAGCLESYTTFNLRLTRDLKYADGNLSLRSTTHPE 180			

Qy	122	PRPRGLHLRQLQAPKESAGCLEASVTFNLFLLTRDLKYVADGNLSLRSTHPE	Db	61	LRLQYRERVALTLKYLEAAAGPALEDTDQPLHTLHILSOLQACIQPQPTA	120
Db	125	PRPRGLHLRQLQAPKESAGCLEASVTFNLFLLTRDLKYVADGNLSLRSTHPE	Qy	121	GPRPGRLHLRQLQAPKESAGCLEASVTNFLLTRDLKYVADGNLSLRSTHPE	180
Qy	182	T 182	Db	121	GPRPGRLHLRQLQAPKESAGCLEASVTNFLLTRDLKYVADGNLSLRSTHPE	180
Db	185	T 185	Qy	181	ST 182	
RESULT 13			Db	181	ST 182	
ADY03662			RESULT 14			
ID ADY03662		standard; protein; 182 AA.	ID AAE18311			
XX			ID AAE18311 standard; protein; 200 AA.			
AC ADY03662;			XX			
XX	05-IBY-2005	(first entry)	AC AAE18311;			
DE Human IL-29 mutant protein sequence SeqID89.			XX			
XX			DT 07-MAY-2002 (first entry)			
KW antiviral; pharmaceutical; hepatitis b virus infection; hepatitis c virus infection; mutant; murine; IL-29.			XX			
XX			DE Human Zcyt21 consensus protein.			
OS Homo sapiens.			XX			
OS Synthetic.			KW Human; interferon like protein; IFN; genetic disease; transgenic animal;			
XX			KW cancer; immune regulation; rheumatoid arthritis; multiple sclerosis;			
US2005037012-A1.			KW myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation;			
XX			KW tumour; viral infection; graft rejection; human immunodeficiency virus; HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;			
PD 17-FEB-2005.			KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive; Zcyt21 protein; chromosome 19q13.13.			
XX			XX			
PF 09-AUG-2004; 2004US-00914772.			OS Homo sapiens.			
PR 07-AUG-2003; 2003US-0493194P.			XX			
PR 10-MAR-2004; 2004US-0551941P.			PN WO200202627-A2.			
PR 02-APR-2004; 2004US-0559142P.			XX			
XX			PD 10-JAN-2002.			
(BRAD/)	BRADY L J.		XX			
PA (KLJIC/)	KLUCHER K M.		PP 29-JUN-2001; 2001WO-US021087.			
PA (CHAN/)	CHAN C.		XX			
PA (DONG/)	DONG D L.		PR 30-JUN-2000; 2000US-0215446P.			
PA (LITCH/)	LIU H Y.		PR 20-APR-2001; 2001US-0288424P.			
PA (SHEPPARD/)	SHEPPARD P O.		XX			
PA (BURO/)	BUKOWSKI T R.		PA (ZYMO ) ZYMOGENETICS INC.			
XX			XX			
Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO, Bukowski TR;	PI Sheepard PO, Prestrell SR, Fox BA, Gilbert T, Haldeman BA;		PI Sheepard PO, Prestrell SR, Fox BA, Gilbert T, Haldeman BA;			
XX			PI Grant FU;			
WPI; 2005-180368/19.	XX		XX			
DR N-PSDB; ADY03661.	PS Disclosure; Page 75; 82pp; English.		DR WPI; 2002-171540/22.			
XX			DR N-PSDB; AAD29546.			
Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.	PT New polypeptide Zcyt21 which is related to interferon, is useful e.g. for treating viral infection and immunological disease.		PT PT			
XX			PT PT			
PT isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.	XX		PT PT			
XX	Claim 1; SEQ ID NO 89; 149pp; English.		XX			
PS			PS Disclosure; Page 75; 82pp; English.			
DR			XX			
N-PSDB;			CC The patent discloses novel polynucleotide and polypeptide molecules for Zcyt21, an interferon (IFN) like protein which is most closely related to INF-alpha. Zcyt21 DNAs are useful for detecting the corresponding genes and its mutants, e.g. for diagnosis of genetic diseases and cancer CC or for detecting chromosome 19 deletions and translocations associated CC with diseases. They are useful for preparing transgenic animals used to CC study the Zcyt21 gene and protein and as antisense inhibitors. Zcyt21 CC sequences and their inhibitors are useful for treating diseases that CC require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis, CC myasthenia gravis, systemic lupus erythematosus and diabetes), tumours, CC inflammation (e.g. arthritis or sepsis), viral infections (e.g. human CC immune deficiency viruses (HIV) and papilloma viruses), graft rejection, CC behavioural and reproductive disorders. They are also used as vaccine CC adjuvants. They can also be used to identify specific inhibitors and CC receptors. The present sequence is human Zcyt21 consensus protein.			
XX	Sequence 182 AA;		CC			
XX	Query Match 99.0%; Score 945; DB 9; Length 182;		CC			
Best Local Similarity 98.9%; Pred. No. 3.1e-90;			CC			
Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			CC			
Qy	1 MGPPVPTSKPTTGKGHGIGRKFKSLSPQELASFKKARDALBSLKLXKWNWSSSPVPGNW	60	CC			
Db	1 MGPPVPTSKPTTGKGHGIGRKFKSLSPQELASFKKARDALBSLKLXKWNWSSSPVPGNW	60	CC			
Qy	61 LRLQYRERVALTLKYLEAAAGPALEDTDQPLHTLHILSOLQACIQPQPTA	120	XX			
SQ	Sequence 200 AA;		SQ			

Query Match 99.0%; Score 945; DB 5; Length 200;  
 Best Local Similarity 99.4%; Pred. No. 3.5e-90;  
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPPTGKGCCHIGRFKSLSPQELASFKKARDALBESLKLNWSSSPVPGNWL 61  
 Db 20 GPvPTSKPPTGKGCCHIGRFKSLSPQELASFKKARDALBESLKLNWSSSPVPGNWL 79

Qy 62 RLLQYRERPVALEAFLATLKVLEAAAGPALEVDQPLHTLHILSQACIOQOPTAG 121  
 Db 80 RLLQYRERPVALEAFLATLKVLEAAAGPALEVDQPLHTLHILSQACIOQOPTAG 139

Qy 122 PRPRGRLAHMLHRLOEAPKESAGLEASVTNFRLRDLKYADGNLSLRSTHPPS 181  
 Db 140 PRPRGRLAHMLHRLOEAPKESAGLEASVTNFRLRDLKYADGNLSLRSTHPPS 199

Qy 182 T 182  
 Db 200 T 200

RESULT 15  
 AAE18310 ID AAE18310 standard; protein; 200 AA.  
 XX AC AAB18310:  
 XX DT 07-MAY-2002 (first entry)  
 XX DE Human Zcyt21 allelic variant protein.  
 XX OS Homo sapiens.  
 XX PN WO200202627-A2.  
 XX PD 10-JAN-2002.  
 XX PF 29-JUN-2001; 2001WO-US021087.  
 XX PR 30-JUN-2000; 2000US-0215446P.  
 XX PR 20-APR-2001; 2001US-0285424P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Sheppard PO, Preneill SR, Fox BA, Gilbert T, Haldeman BA;  
 PI Grant PJ;  
 XX DR WPI; 2002-171640/22.  
 XX DR N-PSBB; AAD29145.  
 PT New polypeptide Zcyt21, which is related to interferon, is useful e.g. for treating viral infection and immunological disease.

Disclosure: Page 72-73; 82pp; English.

PS XX The patent discloses novel polynucleotide and polypeptide molecules for Zcyt21, an interferon (IFN) like protein which is most closely related to INF- $\alpha$ . Zcyt21 DNAs are useful for detecting the corresponding genes and its mutants, e.g. for diagnosis of genetic diseases and cancer or for detecting chromosome 19 deletions and translocations associated with disease. They are useful for preparing transgenic animals used to study the Zcyt21 gene and protein and as antisense inhibitors. Zcyt21 sequences and their inhibitors are useful for treating diseases that require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus and diabetes), tumours,

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OM protein - protein search, using SW model

Run on: December 29, 2005, 13:47:27 ; Search time 46 Seconds

(without alignments)  
327.108 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPPVPTSKPTTGTGCHIGR.....LKTVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:

572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/\_ptodata/1/iaa/5\_COMBO.pep:\*
- 2: /cgn2\_6/\_ptodata/1/iaa/6\_COMBO.pep:\*
- 3: /cgn2\_6/\_ptodata/1/iaa/H\_COMBO.pep:\*
- 4: /cgn2\_6/\_ptodata/1/iaa/PCTUS\_COMBO.pep:\*
- 5: /cgn2\_6/\_ptodata/1/iaa/RE\_COMBO.pep:\*
- 6: /cgn2\_6/\_ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	945	99.0	200	2 US-09-895-834-5	Sequence 5, Appli
2	945	99.0	200	2 US-09-895-834-7	Sequence 7, Appli
3	940	98.4	200	2 US-09-893-737-268	Sequence 268, Appli
4	940	98.4	200	2 US-09-895-834-2	Sequence 2, Appli
5	940	98.4	203	2 US-09-895-834-12	Sequence 12, Appli
6	940	98.4	219	2 US-09-895-834-9	Sequence 9, Appli
7	83	8.7	567	2 US-09-538-092-1365	Sequence 1365, Appli
8	82	8.6	315	2 US-10-370-398-6	Sequence 6, Appli
9	82	8.6	315	2 US-10-080-190-6	Sequence 6, Appli
10	82	8.6	315	2 US-10-082-902-6	Sequence 6, Appli
11	82	8.6	899	2 US-09-958-092-27	Sequence 27, Appli
12	81.5	8.5	1228	2 US-09-252-991A-17764	Sequence 17764, Appli
13	81	8.5	164	2 US-10-104-047-3099	Sequence 3099, Appli
14	80	8.4	563	1 US-08-051-636-2	Sequence 2, Appli
15	80	8.4	563	4 PCT-US94-05268-2	Sequence 2, Appli
16	79	8.3	315	2 US-08-955-903B-8	Sequence 8, Appli
17	79.5	8.3	315	2 US-09-370-398-3	Sequence 3, Appli
18	79.5	8.3	315	2 US-10-080-190-3	Sequence 3, Appli
19	79.5	8.3	315	2 US-10-082-902-3	Sequence 3, Appli
20	79	8.3	495	2 US-09-712-363-181	Sequence 181, Appli
21	79	8.3	903	2 US-09-758-007-1	Sequence 1, Appli
22	79	8.3	1114	2 US-09-637-145-4	Sequence 4, Appli
23	78.5	8.2	378	2 US-09-724-797-40	Sequence 40, Appli
24	78.5	8.2	780	2 US-09-771-161A-144	Sequence 144, Appli
25	78.5	8.2	942	2 US-08-655-852-3	Sequence 3, Appli
26	78.5	8.2	942	2 US-09-771-161A-235	Sequence 235, Appli
27	78.5	8.2	942	2 US-09-771-161A-236	Sequence 236, Appli

RESULT 1  
US-09-895-834-5

; Sequence 5, Application US/09895834

; Parent No. 6327040

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Fox, Brian A.

; APPLICANT: Gilbert, Teresa

; APPLICANT: Halderman, Betty A.

; APPLICANT: Grant, Francis J.

; TITLE OF INVENTION: INTERFRON-LIKE PROTEIN CYTO21

; FILE REFERENCE: 01-18

; CURRENT APPLICATION NUMBER: US/09-895, 834

; PRIORITY APPLICATION NUMBER: 2001-04-29

; PRIOR FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: 60/215, 446

; PRIOR FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSBQ for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 200

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-895-834-5

; Query Match

; Best Local Similarity 99.0%; Score 945; Pred. No. 5 3e-99;

; Mismatches 0; Indels 0;

; Gaps 0;

; Matches 180;

; Conservative 0;

; Scores 180;

; Length 200;

; PCT/KRPTTIGKGCHIGRKFLSISQELASKPKKARDALESLKLKNWCSSPVPGNWDL 61

QY 2 GPVPTRSKPTTIGKGCHIGRKFLSISQELASKPKKARDALESLKLKNWCSSPVPGNWDL 61

QY 2 GPVPTRSKPTTIGKGCHIGRKFLSISQELASKPKKARDALESLKLKNWCSSPVPGNWDL 79

QY 20 GPVPTRSKPTTIGKGCHIGRKFLSISQELASKPKKARDALESLKLKNWCSSPVPGNWDL 79

QY 62 RLLQRRPVALAELALTIVKLEAAAGPALEDVDDQPLTLHILSOLQRCIOPOPTAG 121

QY 80 RLLQRRPVALAELALTIVKLEAAAGPALEDVDDQPLTLHILSOLQRCIOPOPTAG 139

QY 122 PRPRGLRHILRLOEAPKCESAGCLEASYTFNLFRLLTRDLYVADGNLRLRTSHPES 181

QY 140 PRPRGLRHILRLOEAPKCESAGCLEASYTFNLFRLLTRDLYVADGNLRLRTSHPES 199

RESULT 2  
US-09-895-834-7

Sequence 7, Application US/09895834  
 Parent No. 6927040  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Presnell, Scott R.  
 APPLICANT: Fox, Brian A.  
 APPLICANT: Gilbert, Teresa  
 APPLICANT: Haldeiman, Betty A.  
 APPLICANT: Grant, Francis J.  
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYT021  
 CURRENT APPLICATION NUMBER: US/09/895, 834  
 FILE REFERENCE: 01-18  
 PRIORITY FILING DATE: 2001-06-29  
 PRIORITY APPLICATION NUMBER: 60/285, 424  
 PRIORITY FILING DATE: 2001-04-20  
 PRIORITY APPLICATION NUMBER: 60/215, 446  
 PRIORITY FILING DATE: 2000-06-30  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PastSEQ for Windows Version 3.0  
 SEQ ID NO 7  
 LENGTH: 200  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Query Match 99.0%; Score 945; DB 2; Length 200;  
 Best Local Similarity 99.4%; Pred. No. 5 3e-99; Indels 0; Gaps 0;  
 Matches 180; Conservative 0; Mismatches 1; Delins 0; Gap 0;

Qy 2 GPVPTSKPTTGKGCHIGRFKSLSPQELASFKARDALEESLKLKNWCSSPVFPGNWDL 61  
 Db 20 GPVPTSKPTTGKGCHIGRFKSLSPQELASFKARDALEESLKLKNWCSSPVFPGNWDL 79

Qy 62 RLLQVRPVAEALTLKVLEAAGPALEDVQPLTHHILSQLQCIOPTAG 121  
 Db 80 RLLQVRPVAEALTLKVLEAAGPALEDVQPLTHHILSQLQCIOPTAG 139

Qy 122 PRPRGRLHHWLQLQEAQKESAGCLEASVTNLFRLLTRDLYVADGNLSLRSTHPS 181  
 Db 140 PRPRGRLHHWLQLQEAQKESAGCLEASVTNLFRLLTRDLYVADGNLSLRSTHPS 199

Qy 182 T 182  
 Db 200 T 200

RESULT 4  
 US-09-895-834-2  
 ; Sequence 2, Application US/09895834  
 ; Patent No. 6927040  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Fox, Brian A.  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Haldeiman, Betty A.  
 ; APPLICANT: Grant, Francis J.  
 ; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYT021  
 ; FILE REFERENCE: 01-18  
 ; CURRENT APPLICATION NUMBER: US/09/895, 834  
 ; PRIORITY FILING DATE: 2001-06-29  
 ; PRIORITY APPLICATION NUMBER: 60/285, 424  
 ; PRIORITY FILING DATE: 2001-04-20  
 ; PRIORITY APPLICATION NUMBER: 60/215, 446  
 ; PRIORITY FILING DATE: 2000-06-30  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 200  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 98.4%; Score 940; DB 2; Length 200;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-98; Indels 0; Gaps 0;  
 Matches 179; Conservative 1; Mismatches 1; Delins 0; Gap 0;

Qy 2 GPVPTSKPTTGKGCHIGRFKSLSPQELASFKARDALEESLKLKNWCSSPVFPGNWDL 61  
 Db 20 GPVPTSKPTTGKGCHIGRFKSLSPQELASFKARDALEESLKLKNWCSSPVFPGNWDL 79

Qy 62 RLLQVRPVAEALTLKVLEAAGPALEDVQPLTHHILSQLQCIOPTAG 121  
 Db 80 RLLQVRPVAEALTLKVLEAAGPALEDVQPLTHHILSQLQCIOPTAG 139

Qy 122 PRPRGRLHHWLQLQEAQKESAGCLEASVTNLFRLLTRDLYVADGNLSLRSTHPS 181  
 Db 140 PRPRGRLHHWLQLQEAQKESAGCLEASVTNLFRLLTRDLYVADGNLSLRSTHPS 199

Qy 182 T 182  
 Db 200 T 200

RESULT 5  
 US-09-895-834-12  
 ; Sequence 12, Application US/09895834  
 ; Patent No. 6927040  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Fox, Brian A.  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Haldeiman, Betty A.

Query Match 98.4%; Score 940; DB 2; Length 200;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-98; Indels 0; Gaps 0;  
 Matches 179; Conservative 1; Mismatches 1; Delins 0; Gap 0;

Qy 2 GPVPTSKPTTGKGCHIGRFKSLSPQELASFKARDALEESLKLKNWCSSPVFPGNWDL 61

APPLICANT: Grant, Francis J.  
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYT021  
 FILE REFERENCE: 01-18  
 CURRENT APPLICATION NUMBER: US/09/895, 834  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 60/285, 424  
 PRIOR FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: 60/215, 446  
 PRIOR FILING DATE: 2000-06-30  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 12  
 LENGTH: 203  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-895-834-12

Query Match 98.4%; Score 940; DB 2; Length 203;  
 Best Local Similarity 98.9%; Pred. No. 2e-98; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 179; Conservative

Qy 2 GPVPTSKPTTGKCHIGRFKSLSPOEASFKCARDALFESLKLKNWCSSSPVPGNMDL 61  
 Db 23 GPVPTSKPTTGKCHIGRFKSLSPOEASFKCARDALFESLKLKNWCSSSPVPGNMDL 82

Qy 62 RLQVREPPVAELAALTLYKEAAGPALEVDQLHILHILSQLQACTQOPTAG 1.21  
 Db 83 RLQVREPPVAELAALTLYKEAAGPALEVDQLHILHILSQLQACTQOPTAG 142

Qy 122 PRGRGLHHHLRQLQEAKPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRSTTHPES 181  
 Db 143 PRGRGLHHHLRQLQEAKPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRSTTHPES 202

Qy 182 T 182  
 Db 203 T 203

RESULT 6  
 Sequence 9, Application US/0995834  
 Patent No. 692/040  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Presneil, Scott R.  
 APPLICANT: Fox, Brian A.  
 APPLICANT: Gilber, Teresa  
 APPLICANT: Haldeman, Betty A.  
 APPLICANT: Grant, Francis J.  
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYT021  
 FILE REFERENCE: 01-18  
 CURRENT APPLICATION NUMBER: US/09/895, 834  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 60/285, 424  
 PRIOR FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: 60/215, 446  
 PRIOR FILING DATE: 2000-06-30  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 9  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-895-834-9

Query Match 98.4%; Score 940; DB 2; Length 219;  
 Best Local Similarity 98.9%; Pred. No. 2e-98; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 179; Conservative

Qy 2 GPVPTSKPTTGKCHIGRFKSLSPOEASFKCARDALFESLKLKNWCSSSPVPGNMDL 61  
 Db 39 GPVPTSKPTTGKCHIGRFKSLSPOEASFKCARDALFESLKLKNWCSSSPVPGNMDL 98

Qy 62 RLQVREPPVAELAALTLYKEAAGPALEVDQLHILHILSQLQACTQOPTAG 1.21  
 Db 99 RLQVREPPVAELAALTLYKEAAGPALEVDQLHILHILSQLQACTQOPTAG 158

Qy 122 PRGRGLHHHLRQLQEAKPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRSTTHPES 181  
 Db 159 PRGRGLHHHLRQLQEAKPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRSTTHPES 218

Qy 182 T 182  
 Db 219 T 219

RESULT 7  
 Sequence 1365, Application US/09538092  
 Patent No. 6753314  
 GENERAL INFORMATION:  
 APPLICANT: Glot, Loic  
 APPLICANT: Mansfield, Traci A.  
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
 FILE REFERENCE: 15966-542  
 CURRENT APPLICATION NUMBER: US/09/538, 092  
 CURRENT FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: 60/127, 352  
 PRIOR FILING DATE: 1999-04-01  
 PRIOR APPLICATION NUMBER: 60/178, 965  
 PRIOR FILING DATE: 2000-02-01  
 NUMBER OF SEQ ID NOS: 1,387  
 SOFTWARE: CurapateSeqFormatter Version 0.9  
 SEQ ID NO: 1365  
 LENGTH: 567  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (0 .. 10)  
 OTHER INFORMATION: Polypeptide Accession Number Q92696  
 US-09-538-092-1365

Query Match 8.7%; Score 83; DB 2; Length 567;  
 Best Local Similarity 25.6%; Pred. No. 1.4%;  
 Matches 50; Conservative 16; Mismatches 59; Indels 70; Gaps 9;

Qy 25 SPOELASFKKAR-DALEESLKLKNWCSSSPVPGNMDLRLQYERPVAA-LEAELAATLK 82  
 Db 81 SPEELALVKAELGFLSCLRV----NPKSYGTWHRCWLIGRLDEPNWTRELCAR 134

Qy 83 VLE-----AAGPALEVDQLHILHILSQLQACTQOPTAG 117  
 Db 135 FUEVDEENFHCDYRREVATOQAVAPPABELAFTDSLTRNFNYSSHYRSCLPQLRQ 194

Qy 118 PTAGPRGRGL-----HMLHLRQLAEPKKESAGCL-- 147  
 Db 195 PDG-----FQGRLPEDVLLKELELVQNAFFTDPNDQSAWFYHRL--LGRAFDODALRCLHV 250

Qy 148 ---EASYTFNLFRLL 159  
 Db 251 SRDEACLTVSFSRPL 265

RESULT 8  
 Sequence 6, Application US/09370398  
 Patent No. 6423682  
 GENERAL INFORMATION:  
 APPLICANT: Ballinger, Dennis G.  
 APPLICANT: Montgomery, Julie R.  
 TITLE OF INVENTION: Growth Factor Antagonist Materials and Methods  
 FILE REFERENCE: 28110/35878  
 CURRENT APPLICATION NUMBER: US/09/370, 398  
 CURRENT FILING DATE: 1998-08-06  
 NUMBER OF SEQ ID NOS: 13

RESLT 9  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 315  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-370-398-6

Query Match 8.6%; Score 82; DB 2; Length 315;  
 Best Local Similarity 28.6%; Pred. No. 0.79;  
 Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDVLDQPLTLHHLISLQEA-----CLOQPTAGPRPGRGLHHLRLQEA 138  
 Db 28 PDPRDALTQQHVLS-LDQIRAIRNTNEYTEGPTVVRPLKPKAPPSTQHKERHLGL 85

Qy 139 PKKESAGCLEASVTENFLRLLTRDKYVADGN-LSLRSTTHBEST 182  
 Db 86 PEHRQPPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSRTSSSS 130

RESULT 11  
 US-10-090-190-6  
 Sequence 6, Application US/10090190  
 Patent No. 6485920

GENERAL INFORMATION  
 APPLICANT: Ballinger, Dennis G.  
 INVENTION: Growth Factor Antagonist Materials and Methods  
 FILE REFERENCE: 28110/35878  
 CURRENT APPLICATION NUMBER: US/10/090.190  
 CURRENT FILING DATE: 2002-02-04  
 PRIOR APPLICATION NUMBER: US/09/370,398  
 PRIOR FILING DATE: 1998-08-06  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 315  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-090-190-6

Query Match 8.6%; Score 82; DB 2; Length 315;  
 Best Local Similarity 28.6%; Pred. No. 0.79;  
 Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDVLDQPLTLHHLISLQEA-----CLOQPTAGPRPGRGLHHLRLQEA 138  
 Db 28 PDPRDALTQQHVLS-LDQIRAIRNTNEYTEGPTVVRPLKPKAPPSTQHKERHLGL 85

Qy 139 PKKESAGCLEASVTENFLRLLTRDKYVADGN-LSLRSTTHBEST 182  
 Db 86 PEHRQPPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSRTSSSS 130

RESULT 12  
 US-10-082-902-6  
 Sequence 6, Application US/10082902  
 Patent No. 6706871

GENERAL INFORMATION  
 APPLICANT: Ballinger, Dennis G.  
 INVENTION: Growth Factor Antagonist Materials and Methods  
 FILE REFERENCE: 28110/35878  
 CURRENT APPLICATION NUMBER: US/10/082,902  
 CURRENT FILING DATE: 2002-02-26  
 PRIOR APPLICATION NUMBER: US/09/370,398  
 PRIOR FILING DATE: 1998-08-06  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 315  
 TYPE: PRT  
 ORGANISM: Mus musculus

Query Match 8.6%; Score 82; DB 2; Length 315;  
 Best Local Similarity 28.6%; Pred. No. 0.79;  
 Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDVLDQPLTLHHLISLQEA-----CLOQPTAGPRPGRGLHHLRLQEA 138  
 Db 28 PDPRDALTQQHVLS-LDQIRAIRNTNEYTEGPTVVRPLKPKAPPSTQHKERHLGL 85

Qy 139 PKKESAGCLEASVTENFLRLLTRDKYVADGN-LSLRSTTHBEST 182  
 Db 86 PEHRQPPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSRTSSSS 130

RESULT 13  
 US-09-538-092-27  
 Sequence 27, Application US/09538092  
 Patent No. 6753314

GENERAL INFORMATION  
 APPLICANT: Mansfield, Traci A.  
 INVENTION: Protein-Protein Complexes and Method of Using Same  
 FILE REFERENCE: 15966-542  
 CURRENT APPLICATION NUMBER: US/09/538,092  
 CURRENT FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: 60/127,352  
 PRIOR FILING DATE: 1999-04-01  
 PRIOR APPLICATION NUMBER: 60/178,965  
 PRIOR FILING DATE: 2000-02-01  
 NUMBER OF SEQ ID NOS: 1387  
 SOFTWARE: CurapacSeqFormatter Version 0.9  
 SEQ ID NO 27  
 LENGTH: 899  
 TYPE: PRT  
 ORGANISM: Saccharomyces cerevisiae  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (0)..(0)  
 OTHER INFORMATION: Polypeptide Accession Number YBR055C  
 US-09-538-092-27

Query Match 8.6%; Score 82; DB 2; Length 899;  
 Best Local Similarity 22.6%; Pred. No. 3.4;  
 Matches 38; Conservative 27; Mismatches 61; Indels 42; Gaps 8;

Qy 33 KKARDALEESIKLKWKNSCSCSPVPGNWDL-RLLQYR-----PVA 72  
 Db 131 RNRNRRIQEOLNRKYAAPDSLIPRNVDNLKTEREKLQLSQIDENLAQLTKNASNPQI 190

Qy 73 LEABALAT--UKVLEAAAGPALEDVLDQPLTLHHLISLQOACIQOPTAGPRPGRGLHH 130  
 Db 191 VNKPPRATDASLYKLDENDRVNSISDATEDLQKMTLKSRYCADPT---NPQG-----243

RESULT 14  
 US-09-252-991A-17764  
 Sequence 17764, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION  
 APPLICANT: Marc J. Rubenfield et al.  
 INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196-136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US/60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US/60/094,190

Query Match 8.6%; Score 82; DB 2; Length 899;  
 Best Local Similarity 22.6%; Pred. No. 3.4;  
 Matches 38; Conservative 27; Mismatches 61; Indels 42; Gaps 8;

Qy 131 WL--HRLQEAPKKEA-----GCL-----ASVTFNLFRLLTRDKY 165  
 Db 244 WIASARLEEXARKPSVAKKIENGQECPRSSDYLENIRLHESDVHY 291

PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO: 17764  
 LENGTH: 1228  
 TYPE: PRT  
 ORGANISM: *Pseudomonas aeruginosa*  
 FEATURE: LOCATION: (17)  
 NAME/KEY: UNSURE  
 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
 US-09-252-91A-17764

Query Match Score 8.5%; DB 2; Length 1228;  
 Best Local Similarity 33.0%; Pred. No. 5.9;  
 Matches 32; Conservative 5; Mismatches 33; Indels 27; Gaps 5;  
 Qy 56 PGNWDLR-----LQYRERPVVAELALTKVLEAAAGPALEDVLDQPLTLHHL 107  
 Db 738 PGRADLRRPADRRHHLQRRSRVRARRS-----GHARGQA--PVLDAFGHSAH--- 784  
 Qy 1068 SOLQACIQPQ----TAGPRPRGLRLHHMLHRLQEAKP 140  
 Db 785 --LRAAVPQRGHRADRODARRLRLHRYHRLPR 819

RESULT 13  
 US-10-104-047-3099  
 Sequence 3099, Application US/10104047  
 Patent No. 6913241  
 GENERAL INFORMATION  
 APPLICANT: HELIX RESEARCH INSTITUTE  
 TITLE OF INVENTION: No. 6943241e1 full length cDNA  
 CURRENT APPLICATION NUMBER: US/10/104,047  
 FILE REFERENCE: HI-A0105  
 CURRENT FILING DATE: 2002-03-25  
 PRIOR APPLICATION NUMBER:  
 PRIOR FILING DATE:  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3099  
 LENGTH: 164  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-10-104-047-3099

Query Match Score 8.5%; DB 2; Length 164;  
 Best Local Similarity 24.3%; Pred. No. 0.41;  
 Matches 41; Conservative 21; Mismatches 59; Indels 48; Gaps 9;  
 Qy 1 MGPVPTSKPTTIGKCHIGRPFKLSPQLASFKK----ARDALESLKLXWNSCSPVPF 55  
 Db 6 LSPGPVSRVLAAPSCPRG----LLEEECHTLREIILQRCLEEYLR-----PCH 53  
 Qy 56 PGNWDLR---LQYRERPVVAELALTKVLEAAAGPALEDVLDQPLTLHHLSQLA- 112  
 Db 54 PSEAALEPTLAELKEQQAMEQE-----LQASVGPSCV---SPNTRQRPLGSSTQGL 102  
 Qy 113 -----CIOPTAGP----RPGGR--LHHWLHRLQEAQPKKESA 144  
 Db 103 RPPPLPLCGVAVPLQCLPAPPLEPYLRRPGQSATHRGQLQCSPREGPA 151

RESULT 14  
 US-08-061-636-2  
 Sequence 2, Application US/08061636  
 General Information  
 Applicant: Myers, Alan M.  
 Applicant: Madoule, Pascal  
 Title of Invention: Constitutive Pseudohypothal Growth Yeast  
 Title of Invention: Mutants  
 Number of Sequences: 11  
 Correspondence Address:  
 Addressee: Schwegman, Lundberg & Woessner  
 Street: 3500 IDS Center, 80 South Eighth Street  
 City: Minneapolis  
 State: MN USA  
 Zip: 55402  
 Computer Readable Form:  
 Medium Type: Floppy disk  
 Computer: IBM PC compatible  
 Operating System: PC-DOS/MS-DOS  
 Software: PatentIn Release #1.0, Version #1.25

ADDRESSEE: Merchant & Gould  
 STREET: 3100 No. 5855765west Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402-4131  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/061,636  
 FILING DATE: 12-MAY-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mueting, Ann M.  
 REGISTRATION NUMBER: 33,977  
 REFERENCE/DOCKET NUMBER: 9399.38-US01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEFAX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 563 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-061-636-2

Query Match Score 8.4%; DB 1; Length 563;  
 Best Local Similarity 23.5%; Pred. No. 3;  
 Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;  
 Qy 16 CHIGRFKSLSPQELASFKKARDALLESLSKLXWNSCSPVPFPGNMDLRLQYRERYALEA 75  
 Db 319 CHLGNRK-----RDFVTDGEKLDIWSLGVTLY-----CLLYNELPFFGEN 358  
 Qy 76 EIALTUKVLEAA----GAPELDVL-----DOPLHTLHHI 106  
 Db 359 EFETYHKIEVLSLSKINGNTLNDVYKRLLEKDUTLRLISQDLVYLSDQPIDSRNH- 417  
 Qy 107 LSQL-QRCIOPPTAGPPRP--GRFHWHRLQEAQPKKESAG 145  
 Db 418 -SQISSLSSVNPNVPTREGVRRFFGRL-----LTKGKKTSG 452

RESULT 15  
 PCT-US94-05268-2  
 Sequence 2, Application PC/TUS9405268  
 General Information:  
 Applicant: Iowa State University Research Foundation, Inc.  
 Applicant: Institut Pasteur  
 Applicant: Institut National de la Sant et de la Recherche Medicale  
 Applicant: Myerson, Alan M.  
 Applicant: Madoule, Pascal  
 Title of Invention: Constitutive Pseudohypothal Growth Yeast  
 Title of Invention: Mutants  
 Number of Sequences: 11  
 Correspondence Address:  
 Addressee: Schwegman, Lundberg & Woessner  
 Street: 3500 IDS Center, 80 South Eighth Street  
 City: Minneapolis  
 State: MN USA  
 Zip: 55402  
 Computer Readable Form:  
 Medium Type: Floppy disk  
 Computer: IBM PC compatible  
 Operating System: PC-DOS/MS-DOS  
 Software: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05268  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/061,636  
FILING DATE: 12 MAY 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Muetting, Ann M. and Raasch, KC  
REGISTRATION NUMBER: 33,977 and 35,640  
REFERENCE DOCKET NUMBER: 900-38W0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 563 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Search completed: December 29, 2005, 14:00:44

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## OM protein - protein search, using sw model

Run on: December 29, 2005, 13:59:18 ; Search time 164 Seconds

(without alignments)  
463.689 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPVPTSKPPTTGKGCHIGR.....LKYVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:

1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\*

Maximum Match 100%

## Listing first 45 summaries

Database : Published Applications AA Main:  
 1: /cnr2\_6\_ptodata/1/pubpaas/US07\_PUBCOMB\_pep:  
 2: /cnr2\_6\_ptodata/1/pubpaas/US08\_PUBCOMB\_pep:  
 3: /cnr2\_6\_ptodata/1/pubpaas/US09\_PUBCOMB\_pep:  
 4: /cnr2\_6\_ptodata/1/pubpaas/US10A\_PUBCOMB\_pep:  
 5: /cnr2\_6\_ptodata/1/pubpaas/US10B\_PUBCOMB\_pep:  
 6: /cnr2\_6\_ptodata/1/pubpaas/US11\_PUBCOMB\_pep:  
 \* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	955	100.0	182	4	US-10-691-923-34	Sequence 34, App1
2	955	100.0	182	5	US-10-914-772-29	Sequence 29, App1
3	951	99.6	182	5	US-10-914-772-41	Sequence 41, App1
4	950	99.5	181	4	US-10-691-923-32	Sequence 32, App1
5	950	99.5	181	5	US-10-914-772-27	Sequence 27, App1
6	950	99.5	182	4	US-10-691-923-38	Sequence 38, App1
7	950	99.5	182	5	US-10-914-772-15	Sequence 15, App1
8	948	99.3	183	5	US-10-914-772-15	Sequence 155, App1
9	947	99.2	183	5	US-10-914-772-155	Sequence 40, App1
10	946	99.1	181	5	US-10-914-772-40	Sequence 85, App1
11	946	99.1	182	5	US-10-914-772-85	Sequence 161, App1
12	946	99.1	185	5	US-10-914-772-161	Sequence 89, App1
13	945	99.0	182	5	US-10-914-772-89	Sequence 5, App1
14	945	99.0	200	3	US-09-895-834-5	Sequence 7, App1
15	945	99.0	200	4	US-09-895-834-7	Sequence 20, App1
16	945	99.0	200	4	US-10-691-923-20	Sequence 5, App1
17	945	99.0	200	4	US-10-790-996-5	Sequence 7, App1
18	945	99.0	200	4	US-10-790-996-7	Sequence 5, App1
19	945	99.0	200	5	US-10-928-539-5	Sequence 7, App1
20	945	99.0	200	5	US-10-928-539-7	Sequence 4, App1
21	945	99.0	200	5	US-10-914-772-4	Sequence 5, App1
22	945	99.0	200	5	US-10-927-891-5	Sequence 7, App1
23	945	99.0	200	5	US-10-927-891-7	Sequence 5, App1
24	945	99.0	200	5	US-10-927-815-5	Sequence 7, App1
25	945	99.0	200	5	US-10-927-815-7	Sequence 10, App1
26	944	98.8	182	5	US-10-914-772-05	Sequence 83, App1
27	941	98.5	181	5	US-10-914-772-83	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	955	100.0	182	4	US-10-691-923-34	Sequence 34, App1
2	955	100.0	182	5	US-10-914-772-29	Sequence 29, App1
3	951	99.6	182	5	US-10-914-772-41	Sequence 41, App1
4	950	99.5	181	4	US-10-691-923-32	Sequence 32, App1
5	950	99.5	181	5	US-10-914-772-27	Sequence 27, App1
6	950	99.5	182	4	US-10-691-923-38	Sequence 38, App1
7	950	99.5	182	5	US-10-914-772-15	Sequence 15, App1
8	948	99.3	183	5	US-10-914-772-15	Sequence 155, App1
9	947	99.2	183	5	US-10-914-772-155	Sequence 40, App1
10	946	99.1	181	5	US-10-914-772-40	Sequence 85, App1
11	946	99.1	182	5	US-10-914-772-85	Sequence 161, App1
12	946	99.1	185	5	US-10-914-772-161	Sequence 89, App1
13	945	99.0	182	5	US-10-914-772-89	Sequence 5, App1
14	945	99.0	200	3	US-09-895-834-5	Sequence 7, App1
15	945	99.0	200	4	US-09-895-834-7	Sequence 20, App1
16	945	99.0	200	4	US-10-691-923-20	Sequence 5, App1
17	945	99.0	200	4	US-10-790-996-5	Sequence 7, App1
18	945	99.0	200	4	US-10-790-996-7	Sequence 5, App1
19	945	99.0	200	5	US-10-928-539-5	Sequence 7, App1
20	945	99.0	200	5	US-10-928-539-7	Sequence 4, App1
21	945	99.0	200	5	US-10-914-772-4	Sequence 5, App1
22	945	99.0	200	5	US-10-927-891-5	Sequence 7, App1
23	945	99.0	200	5	US-10-927-891-7	Sequence 5, App1
24	945	99.0	200	5	US-10-927-815-5	Sequence 7, App1
25	945	99.0	200	5	US-10-927-815-7	Sequence 10, App1
26	944	98.8	182	5	US-10-914-772-05	Sequence 83, App1
27	941	98.5	181	5	US-10-914-772-83	

## ALIGNMENTS

RESULT 1  
 US-10-691-923-34  
 ; Sequence 34, Application US-10691923  
 ; Publication No. US20040138122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Klucher, Kevin M.  
 ; APPLICANT: Sivakumar, Pallavur V.  
 ; APPLICANT: Kinsbogel, Wayne R.  
 ; APPLICANT: Henderson, Katherine E.  
 ; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION  
 ; TITLE OF INVENTION: USING IL-28 AND IL-29  
 ; CURRENT APPLICATION NUMBER: US/10/691,923  
 ; CURRENT FILING DATE: 2003-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/420,714  
 ; PRIOR FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/463,939  
 ; PRIOR FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: US 60/420,713  
 ; PRIOR FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/453,982  
 ; PRIOR FILING DATE: 2003-04-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 34  
 ; LENGTH: 182  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: met IL-29 mutant C172S  
 ; US-10-691-923-34

Query Match Score 955; DB 4; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-86;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MGPPVTSKPTTICKGCHIGRKFSKQELASPKKARDALESLKLKNWSQLQACTQPQTA 120  
 Db 1 MGPPVTSKPTTICKGCHIGRKFSKQELASPKKARDALESLKLKNWSQLQACTQPQTA 120  
 Qy 1 LRLJQVRERPVAAELALTLKVLAAGPALEVDLDOPPLTHHLISQLQACTQPQTA 120  
 Db 1 LRLJQVRERPVAAELALTLKVLAAGPALEVDLDOPPLTHHLISQLQACTQPQTA 120  
 121 GPRGRGLHHWHLHQQLQAPKKESAGCLESVTNLFRLLTDKYYAVDGNLSLRTSTHPE 180  
 121 GPRGRGLHHWHLHQQLQAPKKESAGCLESVTNLFRLLTDKYYAVDGNLSLRTSTHPE 180  
 181 ST 182

Db 181 ST 182

**RESULT 2**  
 US-10-914-772-29  
 Sequence 29, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 APPLICANT: Brady, Lowell J.  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Chan, Chung  
 APPLICANT: Dong, Dennis L.  
 APPLICANT: Liu, Hong Y.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Bukowski, Thomas R.  
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772  
 CURRENT FILING DATE: 2004-03-09  
 PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIORITY FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIORITY FILING DATE: 2004-03-10  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 PRIORITY FILING DATE: 2004-04-02  
 NUMBER OF SEQ ID NOS: 161  
 SEQ ID NO 29  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: met IL-29 mutant C172X

Query Match 99.6%; Score 951; DB 5; Length 182;  
 Best Local Similarity 99.5%; Pred. No. 3.e-86;  
 Matches 181; Conservative 0; Mismatches -1; Indels 0; Gaps 0;

Qy 1 MGPPVTSKPTTGGCHIGRKSLSPQELASPKKARDALESSLKLKNWCSPPVFPGNWD 60  
 Db 1 MGPPVTSKPTTGGCHIGRKSLSPQELASPKKARDALESSLKLKNWCSPPVFPGNWD 60

Qy 61 LRLLQVRERPVAEELALTLLKYLEAAAGPALEDVLDQPLTLHHLISQLQACIQOPTA 120  
 Db 61 LRLLQVRERPVAEELALTLLKYLEAAAGPALEDVLDQPLTLHHLISQLQACIQOPTA 120

Qy 61 GPRGRGLAHWHLRQEAQKCESAGCLESATVNFLRLLTDLKTYADGNLSLRSTHPE 180  
 Db 61 GPRGRGLAHWHLRQEAQKCESAGCLESATVNFLRLLTDLKTYADGNLSLRSTHPE 180

Qy 181 ST 182  
 Db 181 ST 182

**RESULT 3**  
 US-10-914-772-41  
 Sequence 41, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 APPLICANT: Brady, Lowell J.  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Chan, Chung  
 APPLICANT: Dong, Dennis L.  
 APPLICANT: Liu, Hong Y.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Bukowski, Thomas R.  
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772

Query Match 99.6%; Score 951; DB 5; Length 182;  
 Best Local Similarity 99.5%; Pred. No. 3.e-86;  
 Matches 181; Conservative 0; Mismatches -1; Indels 0; Gaps 0;

Qy 1 MGPPVTSKPTTGGCHIGRKSLSPQELASPKKARDALESSLKLKNWCSPPVFPGNWD 60  
 Db 1 MGPPVTSKPTTGGCHIGRKSLSPQELASPKKARDALESSLKLKNWCSPPVFPGNWD 60

Qy 61 LRLLQVRERPVAEELALTLLKYLEAAAGPALEDVLDQPLTLHHLISQLQACIQOPTA 120  
 Db 61 LRLLQVRERPVAEELALTLLKYLEAAAGPALEDVLDQPLTLHHLISQLQACIQOPTA 120

Qy 121 GPRGRGLAHWHLRQEAQKCESAGCLESATVNFLRLLTDLKTYAVAGNLSRTSHP 180  
 Db 121 GPRGRGLAHWHLRQEAQKCESAGCLESATVNFLRLLTDLKTYAVAGNLSRTSHP 180

Qy 181 ST 182  
 Db 181 ST 182

**RESULT 4**  
 US-10-691-923-32  
 Sequence 32, Application US/10691923  
 Publication No. US20040138122A1  
 GENERAL INFORMATION:  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Sivakumar, Pallavur V.  
 APPLICANT: Kindbogel, Wayne R.  
 APPLICANT: Henderson, Katherine E.  
 TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION  
 FILE REFERENCE: 02-24  
 CURRENT APPLICATION NUMBER: US/10/691,923  
 CURRENT FILING DATE: 2003-10-23  
 PRIOR APPLICATION NUMBER: US 60/420,714  
 PRIOR FILING DATE: 2002-10-23  
 PRIOR APPLICATION NUMBER: US 60/463,939  
 PRIOR FILING DATE: 2003-04-18  
 PRIOR APPLICATION NUMBER: US 60/420,713  
 PRIOR FILING DATE: 2002-10-23  
 PRIOR APPLICATION NUMBER: US 60/463,982  
 NUMBER OF SEQ ID NOS: 40  
 SOFTWARE: Fast-SEQ for Windows Version 4.0  
 SEQ ID NO 32  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: IL-29 mutant C171S

US-10-691-923-32

Query Match 99.5%; Score 950; DB 4; Length 181;  
 Best Local Similarity 100.0%; Prd. No. 4.3e-06;  
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 US-10-691-923-38  
 / Sequence 38, Application US/10691923  
 / Publication No. US20040138122A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Klucher, Kevin M.  
 / APPLICANT: Sivakumar, Pallavur V.  
 / APPLICANT: Kindvogel, Wayne R.  
 / APPLICANT: Henderson, Katherine E.  
 / TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION  
 / TITLE OF INVENTION: USING IL-28 AND IL-29  
 / FILE REFERENCE: 02-24  
 / CURRENT APPLICATION NUMBER: US/10/691-923  
 / CURRENT FILING DATE: 2003-10-23  
 / PRIOR APPLICATION NUMBER: US 60/420,714  
 / PRIOR FILING DATE: 2002-10-23  
 / PRIOR APPLICATION NUMBER: US 60/463,939  
 / PRIOR FILING DATE: 2003-04-18  
 / PRIOR APPLICATION NUMBER: US 60/420,713  
 / PRIOR FILING DATE: 2003-10-23  
 / PRIOR APPLICATION NUMBER: US 60/463,982  
 / PRIOR FILING DATE: 2003-04-18  
 / NUMBER OF SEQ ID NOS: 40  
 / SOFTWARE: FastSEQ for Windows Version 4.0  
 / SEQ ID NO 38  
 / LENGTH: 182  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: met IL-29  
 US-10-691-923-38

Query Match 99.5%; Score 950; DB 4; Length 182;  
 Best Local Similarity 99.5%; Prd. No. 4.3e-06;  
 Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7  
 US-10-14-772-15  
 / Sequence 15, Application US/10914772  
 / Publication No. US200500317012A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Brady, Lowell J.  
 / APPLICANT: Klucher, Kevin M.  
 / APPLICANT: Chan, Chung  
 / APPLICANT: Dong, Dennis L.  
 / APPLICANT: Liu, Hong Y.  
 / APPLICANT: Sheppard, Paul O.  
 / APPLICANT: Bukowski, Thomas R.  
 / TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 / TITLE OF INVENTION: IL-29  
 / FILE REFERENCE: 03-10  
 / CURRENT APPLICATION NUMBER: US/10/914,772  
 / CURRENT FILING DATE: 2004-01-09  
 / PRIOR APPLICATION NUMBER: US 60/493,194  
 / PRIOR FILING DATE: 2003-08-07  
 / PRIOR APPLICATION NUMBER: US 60/551,841  
 / PRIOR FILING DATE: 2004-03-10  
 / PRIOR APPLICATION NUMBER: US 60/559,142  
 / PRIOR FILING DATE: 2004-04-02  
 / NUMBER OF SEQ ID NOS: 161  
 / SOFTWARE: FastSEQ for Windows Version 4.0  
 / SEQ ID NO 27  
 / LENGTH: 181  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: IL-29 mutant C171S  
 US-10-914-772-27

Query Match 99.5%; Score 950; DB 5; Length 181;  
 Best Local Similarity 100.0%; Prd. No. 4.3e-06;  
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 US-10-14-772-15  
 / Sequence 15, Application US/10914772  
 / Publication No. US200500317012A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Brady, Lowell J.  
 / APPLICANT: Klucher, Kevin M.  
 / APPLICANT: Chan, Chung  
 / APPLICANT: Dong, Dennis L.  
 / APPLICANT: Liu, Hong Y.  
 / APPLICANT: Sheppard, Paul O.  
 / APPLICANT: Bukowski, Thomas R.  
 / TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 / TITLE OF INVENTION: IL-29  
 / FILE REFERENCE: 03-10  
 / CURRENT APPLICATION NUMBER: US/10/914,772  
 / CURRENT FILING DATE: 2004-08-09

Query Match 99.5%; Score 950; DB 5; Length 181;  
 Best Local Similarity 100.0%; Prd. No. 4.3e-06;  
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 US-10-914-772-27

PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIOR FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 PRIOR FILING DATE: 2004-03-10  
 NUMBER OF SEQ ID NOS: 161  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 15  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: mature protein of SEQ ID NO: 3, with 3' Met added  
 US-10-914-772-15

Query Match 99.5%; Score 950; DB 5; Length 182;  
 Best Local Similarity 99.5%; Pred. No. 4.3e-86;  
 Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEEFSLKLKNWCSSSPVPFGNWD 60  
 Db 1 MGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEEFSLKLKNWCSSSPVPFGNWD 60

RESULT 9  
 US-10-914-772-155  
 Sequence 155, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 / APPLICANT: Brady, Lowell J.  
 / APPLICANT: Klucher, Kevin M.  
 / APPLICANT: Chan, Chung  
 / APPLICANT: Dong, Dennis L.  
 / APPLICANT: Liu, Hong Y.  
 / APPLICANT: Sheppard, Paul O.  
 / APPLICANT: Bukowski, Thomas R.  
 / TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 / FILE REFERENCE: IL-29  
 / CURRENT APPLICATION NUMBER: US/10/914,772  
 / CURRENT FILING DATE: 2004-08-09  
 / PRIORITY NUMBER: US 60/493,194  
 / PRIOR FILING DATE: 2003-08-07  
 / PRIORITY NUMBER: US 60/551,841  
 / PRIOR FILING DATE: 2004-03-10  
 / PRIORITY NUMBER: US 60/559,142  
 / PRIOR FILING DATE: 2004-04-02  
 / NUMBER OF SEQ ID NOS: 161  
 / SEQ ID NO: 155  
 / SOFTWARE: FastSEQ for Windows Version 4.0  
 / LENGTH: 183  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: IL-29 file insert after N-terminal Met, C173X

FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772  
 CURRENT FILING DATE: 2004-08-09  
 PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIOR FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIOR FILING DATE: 2004-03-10  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 NUMBER OF SEQ ID NOS: 161  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 151  
 LENGTH: 183  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: IL-29 Leu insert after N-terminal Met, C173X  
 / NAME/KEY: VARIANT  
 / LOCATION: (173) .. (173)  
 / OTHER INFORMATION: xaa = Ser, Ala, Thr, Val, or Asn  
 US-10-914-772-155

Query Match 99.2%; Score 947; DB 5; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.6e-86;  
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEEFSLKLKNWCSSSPVPFGNWD 60  
 Db 2 IGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEEFSLKLKNWCSSSPVPFGNWD 61

RESULT 10  
 US-10-914-772-156  
 Sequence 156, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 / APPLICANT: Brady, Lowell J.  
 / APPLICANT: Klucher, Kevin M.  
 / APPLICANT: Chan, Chung  
 / APPLICANT: Dong, Dennis L.  
 / APPLICANT: Liu, Hong Y.  
 / APPLICANT: Sheppard, Paul O.  
 / APPLICANT: Bukowski, Thomas R.  
 / TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 / FILE REFERENCE: 03-10  
 / CURRENT APPLICATION NUMBER: US/10/914,772  
 / CURRENT FILING DATE: 2004-08-09  
 / PRIORITY NUMBER: US 60/493,194  
 / PRIOR FILING DATE: 2003-08-07  
 / PRIORITY NUMBER: US 60/551,841  
 / PRIOR FILING DATE: 2004-03-10  
 / PRIORITY NUMBER: US 60/559,142  
 / PRIOR FILING DATE: 2004-04-02  
 / NUMBER OF SEQ ID NOS: 161  
 / SEQ ID NO: 156  
 / SOFTWARE: FastSEQ for Windows Version 4.0  
 / LENGTH: 183  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: IL-29 file insert after N-terminal Met, C173X

FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772  
 CURRENT FILING DATE: 2004-08-09  
 PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIOR FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIOR FILING DATE: 2004-03-10  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 NUMBER OF SEQ ID NOS: 161  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 151  
 LENGTH: 183  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: IL-29 Leu insert after N-terminal Met, C173X  
 / NAME/KEY: VARIANT  
 / LOCATION: (173) .. (173)  
 / OTHER INFORMATION: xaa = Ser, Ala, Thr, Val, or Asn  
 US-10-914-772-156

Db 122 GPRGRGLHHLRQLQEPKESAGCLEASVTNFLRDLKYVAOGNLXLRSTHPE 181  
 Qy 181 ST 182  
 Db 182 ST 183

---

RESULT 9 10  
 US-10-914-772-40  
 Sequence 40, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 APPLICANT: Brady, Lowell J.  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Chan, Chung  
 APPLICANT: Dong, Dennis L.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Bukowski, Thomas R.  
 APPLICANT: Liu, Hong Y.  
 APPLICANT: Li, Hong Y.  
 APPLICANT: Sherppard, Paul O.  
 APPLICANT: Dennis L.  
 APPLICANT: Kevin M.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan  
 APPLICANT: Lowell J.  
 APPLICANT: Lowell J.  
 APPLICANT: Kevin M.  
 APPLICANT: Dennis L.  
 APPLICANT: Paul O.  
 APPLICANT: Thomas R.  
 APPLICANT: Hong Y.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Bukowski, Thomas R.  
 APPLICANT: Dennis L.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan  
 APPLICANT: Lowell J.  
 APPLICANT: Kevin M.  
 APPLICANT: Dennis L.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Thomas R.  
 APPLICANT: Hong Y.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan

TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772  
 CURRENT FILING DATE: 2004-08-09  
 PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIOR FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIOR FILING DATE: 2004-03-10  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 PRIOR FILING DATE: 2004-04-02  
 NUMBER OF SEQ ID NOS: 161  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 85  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Met IL29 mutant Asp170, C172X  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (172) .. (172)  
 OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
 US-10-914-772-85

Query Match 99.1%; Score 946; DB 5; Length 182;  
 Best Local Similarity 98.9%; Pred. No. 1..1e-85;  
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGVPPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESIILKWNWCSSPVPGNWD 60  
 Db 1 MGVPPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESIILKWNWCSSPVPGNWD 60

Qy 61 LRLLQVRERPVVALEELALTLKVLEAAGPALEDVLDQPLHTLHHSLSQACTQPQPTA 120  
 Db 61 LRLLQVRERPVVALEELALTLKVLEAAGPALEDVLDQPLHTLHHSLSQACTQPQPTA 120

Qy 121 GPRGRGLHHLRQLQEPKESAGCLEASVTNFLRDLKYVAOGNLXLRSTHPE 180  
 Db 121 GPRGRGLHHLRQLQEPKESAGCLEASVTNFLRDLKYVAOGNLXLRSTHPE 180

RESULT 12  
 US-10-914-772-161  
 Sequence 161, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 APPLICANT: Brady, Lowell J.  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Chan, Chung  
 APPLICANT: Dong, Dennis L.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Bukowski, Thomas R.  
 APPLICANT: Dennis L.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan  
 APPLICANT: Lowell J.  
 APPLICANT: Kevin M.  
 APPLICANT: Dennis L.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Thomas R.  
 APPLICANT: Hong Y.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan  
 APPLICANT: Lowell J.  
 APPLICANT: Kevin M.  
 APPLICANT: Dennis L.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Thomas R.  
 APPLICANT: Hong Y.  
 APPLICANT: Kevin M.  
 APPLICANT: Chung, Chan

TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND  
 FILE REFERENCE: 03-10  
 CURRENT APPLICATION NUMBER: US/10/914,772  
 CURRENT FILING DATE: 2004-08-09  
 PRIOR APPLICATION NUMBER: US 60/493,194  
 PRIOR FILING DATE: 2003-08-07  
 PRIOR APPLICATION NUMBER: US 60/551,841  
 PRIOR FILING DATE: 2004-03-10  
 PRIOR APPLICATION NUMBER: US 60/559,142  
 PRIOR FILING DATE: 2004-04-02

RESULT 11  
 US-10-914-772-85  
 Sequence 85, Application US/10914772  
 Publication No. US20050037012A1  
 GENERAL INFORMATION:  
 APPLICANT: Brady, Lowell J.  
 APPLICANT: Klucher, Kevin M.  
 APPLICANT: Chung, Chan

NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 161  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal  
; OTHER INFORMATION: Met, C17X  
; FEATURE: NAME/KEY: VARIANT  
; LOCATION: (175) .. (175)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
; us-10-914-772-161

Query Match Score 945; DB 5; Length 182;  
Best Local Similarity 98.4%; Pred. No. 1.4e-85;  
Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGVPITSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWD 60  
Db 1 MGVPITSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWD 60

Qy 61 RLQLQERPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSQLACIQOPTA 120  
Db 61 RLQLQERPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSQLACIQOPTA 120

Qy 121 GPRGRGLHHMHLRLQEAQPKESAGCLESVTNLFRLLTRDLYADGNLSLRSTHPE 180  
Db 121 GPRGRGLHHMHLRLQEAQPKESAGCLESVTNLFRLLTRDLYADGNLSLRSTHPE 180

Query Match Score 946; DB 5; Length 185;  
Best Local Similarity 99.4%; Pred. No. 1.1e-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 181 ST 182

Qy 181 ST 182

Qy 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWDL 61  
Db 5 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWDL 64

RESULT 14  
US-09-895-834-5  
; Sequence 5, Application US/09895834  
; Publication No. US2002003973A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Haldeiman, Betty A.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN CYTO21  
; FILE REFERENCE: 01-18

CURRENT APPLICATION NUMBER: US/09/895, 834  
CURRENT FILING DATE: 2003-06-29  
PRIOR APPLICATION NUMBER: 60/285, 424  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/215, 446  
PRIOR FILING DATE: 2000-06-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 200  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-895-834-5

Query Match Score 945; DB 3; Length 200;  
Best Local Similarity 99.4%; Pred. No. 1.5e-85;  
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWDL 61  
Db 20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLKNWCSSSPVPFGNWDL 79

Qy 62 RLQLQERPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSQLACIQOPTAG 121  
Db 80 RLQLQERPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSQLACIQOPTAG 139

Qy 122 PRPRGRGLHHMHLRLQEAQPKESAGCLESVTNLFRLLTRDLYADGNLSLRSTHPE 181  
Db 140 PRPRGRGLHHMHLRLQEAQPKESAGCLESVTNLFRLLTRDLYADGNLSLRSTHPE 199

RESULT 15  
US-09-895-834-7  
; Sequence 7, Application US/09895834  
; Publication No. US2002003973A1

OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
; OTHER INFORMATION: Met IL29 mutant Trp, Asn170, C172X  
; FEATURE: NAME/KEY: VARIANT  
; LOCATION: (172) .. (172)  
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn  
; us-10-914-772-89

GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Presnell, Scott R.  
 APPLICANT: Fox, Brian A.  
 APPLICANT: Gilbert, Teresa  
 APPLICANT: Haldeeman, Betty A.  
 APPLICANT: Grant, Francis J.  
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21  
 FILE REFERENCE: 01-18  
 CURRENT APPLICATION NUMBER: US/09/895, 834  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 60/285, 424  
 PRIOR FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: 60/215, 446  
 PRIOR FILING DATE: 2000-06-30  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 7  
 LENGTH: 200  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-895-834-7

	Query Match	Score	DB	Length
Qy	Best Local Similarity 99.0%	945	3	200;
Qy	Matches 180; Conservative	Pred. No. 1.5e-85;		
Qy	Mismatches 0;	Indels 1;		
Qy	GPIPTSKPTTGKCHIGPKLSPQEELSKKKARDALBESIILKLNWQKCCSSPVPGNIDL	61		
Db	20 GIVPTSKPTTGKCHIGPKLSPQEELSKKKARDALBESIILKLNWQKCCSSPVPGNIDL	79		
Qy	62 RLLQVRERPVALEELAFTLKVLAAGPALEVDVLDQPLHTLHISLQLQACIQOPPAG	121		
Db	80 RLLQVRERPVALEELAFTLKVLAAGPALEVDVLDQPLHTLHISLQLQACIQOPPAG	139		
Qy	122 PRPRGRLLHHLRLOEAKKESEAGCLEASYTFNLFRLLTRDLKYVADGNLSRTSTHPS	181		
Db	140 PRPRGRLLHHLRLOEAKKESEAGCLEASYTFNLFRLLTRDLKYVADGNLCRTSTHPS	199		
Qy	182 T 182			
Db	200 T 200			

Search completed: December 29, 2005, 14:13:28  
 Job time : 165 secs